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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:02:07 ; Search time 16.5871 Seconds
(without alignments)
3219.466 Million cell updates/sec

Title: US-09-830-972-2_COPY_975_1163
Perfect score: 925
Sequence: 1 S V V D L L Y W R D I K K T G V V F G A V K D A M A K I Q A K I P G L K R K A D 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	925	100.0	361	3	AAY71385	Aay71385 Alternati
2	925	100.0	1163	3	AAY71310	Aay71310 Rat neuri
3	925	100.0	1163	3	AAY71384	Aay71384 Alternati
4	925	100.0	1163	5	ABB81074	Abb81074 Rat neuro
5	922	99.7	379	7	ADB85283	Adb85283 Rat fooce
6	921	99.6	199	5	ABB81077	Abb81077 Rat neuro
7	921	99.6	360	3	AAY71383	Aay71383 Rat neuri
8	921	99.6	360	5	ABB81076	Abb81076 Rat neuro
9	921	99.6	522	3	AAY71312	Aay71312 Rat neuri

10	919	99.4	199	3	AAV71559	Aay71559	Rat	Nogo
11	919	99.4	359	3	AAV71558	Aay71558	Rat	Nogo
12	919	99.4	403	3	AAV71563	Aay71563	Rat	Nogo
13	919	99.4	1162	3	AAV71557	Aay71557	Rat	Nogo
14	908	98.2	893	3	AAV95012	Aay95012	Human	sec
15	908	98.2	983	6	ABU11573	Abu11573	Human	MDD
16	908	98.2	1178	3	AAV71311	Aay71311	Human	neu
17	908	98.2	1192	3	AAV56967	Aay56967	Human	MAG
18	908	98.2	1192	4	AAB82349	Aab82349	Human	NOG
19	908	98.2	1192	4	AAU04591	Aau04591	Human	Nog
20	908	98.2	1192	5	ABG30938	Abg30938	Human	Nog
21	908	98.2	1192	5	ABP68600	Abp68600	Human	pan
22	908	98.2	1192	5	ABB81078	Abb81078	Human	neu
23	908	98.2	1192	6	ABR59667	Abr59667	Human	Nog
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25	904	97.7	199	2	AAW53947	Aaw53947	Human	NSP
26	904	97.7	199	2	AAW78313	Aaw78313	Fragment	
27	904	97.7	199	3	AAB12805	Aab12805	Human	NSP
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29	904	97.7	199	5	ABB81080	Abb81080	Human	neu
30	904	97.7	373	3	AAV53624	Aay53624	A	bone ma
31	904	97.7	373	3	AAV56969	Aay56969	Human	MAG
32	904	97.7	373	3	AAB24242	Aab24242	Human	Nog
33	904	97.7	373	4	AAB82350	Aab82350	Human	NOG
34	904	97.7	373	5	AAM47954	Aam47954	Human	RTN
35	904	97.7	373	5	ABG30937	Abg30937	Human	Nog
36	904	97.7	373	5	ABP68601	Abp68601	Human	pan
37	904	97.7	373	5	ABB81079	Abb81079	Human	neu
38	900	97.3	291	4	AAM93484	Aam93484	Human	pol
39	895	96.8	199	2	AAV35903	Aay35903	Extended	
40	871.5	94.2	642	2	AAW58383	Aaw58383	Human	sec
41	871.5	94.2	642	4	AAB90682	Aab90682	Human	BG1
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45	679	73.4	208	3	AAB12808	Aab12808	NSPC	prot

ALIGNMENTS

RESULT 1

AAY71385

ID AAY71385 standard; protein; 361 AA.

XX

AC AAY71385;

XX

DT 02-NOV-2000 (first entry)

XX

DE Alternative version of rat neurite growth inhibitor Nogo B.

XX

KW Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Region 1. .172
FT /note= "Corresponds to amino acids 1-172 of Nogo A
FT protein shown in AAY71310"
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FT /note= "Inhibits NIH 3T3 fibroblast spreading"
FT Modified-site 30
FT /note= "Casein kinase II site"
FT Region 31. .58
FT /note= "Acidic region"
FT Region 173. .361
FT /note= "Corresponds to amino acids 975-1163 of Nogo A
FT protein (AAY71310)"
FT Region 174. .361
FT /note= "This region is common to Nogo A, B and C
FT isoforms"
FT Domain 186. .221
FT /label= Transmembrane_domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 222
FT /note= "Protein kinase C (PKC) site"
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FT /note= "Asn is N-glycosylated"
FT Modified-site 271
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 287
FT /note= "Protein kinase C (PKC) site"
FT Domain 288. .323
FT /label= Transmembrane_domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 339. .341
FT /note= "Asn is N-glycosylated"
FT Modified-site 341
FT /note= "Protein kinase C (PKC) site"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX

PS Claim 4; Page; 122pp; English.

xx

The present sequence is an alternative version of rat Nogo B protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The Nogo B transcript arises as a result of alternative splicing of Nogo gene. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendrolioma, menangioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS.

Note: The present sequence is not given in the specification but is derived from Nogo A protein sequence (AAV71310) and corresponds to residues 1-172 fused to 975-1163 of Nogo A. This sequence is an alternative version of the Nogo B sequence (see AAV71383) described in the specification as being residues 1-172 fused to C-terminal 188 amino acids (residues 976-1163) of Nogo A. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers

xx

SO Sequence 361 AA;

Query Match 100.0%; Score 925; DB 3; Length 361;
Best Local Similarity 100.0%; Pred. No. 8.7e-90;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV

1 SVVDILLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60

D_b

173 SVVDLILYWRDIKKTGVVFASLFLLLSLTVESIVSVTAYIALALLSVTISERIYKGVIOA 232

Ov

61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAV 120

Ph

233 IOKSDEGHPFRAYLESEVAISEELVOKYSNSALGHVNSTIKELRRLFLVDDLVDSLKF 294

Qv

121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHGLANKSVKDAMAKIQAK 180

Dh

293 LMWVFTYVGAIENGLTILLIALLISIESTPVYERHOVTDHYLGLANKSVKDAKAKIAK 352

Qv

181 IPGLKRKAD 189

27

THE INSTITUTE 215

RESULT 3

RESULT 2

ID: AAX71310 standard; protein: 1163 AA

10

AC AAY71310;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat neurite growth inhibitor Nogo A.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Inhibitory-site 1. .171
FT /note= "Inhibits NIH 3T3 fibroblast spreading"
FT Modified-site 30
FT /note= "Casein kinase II site"
FT Region 31. .58
FT /note= "Acidic region"
FT Region 31. .57
FT /note= "Region specifically described in claim 16"
FT Region 172. .259
FT /note= "This region is not essential for inhibitory
FT activity"
FT Modified-site 233
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 242. .244
FT /note= "Asn is N-glycosylated"
FT Modified-site 291
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 295
FT /note= "Protein kinase C (PKC) site"
FT Misc-difference 404
FT /note= "Encoded by TTG"
FT Modified-site 436
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 468. .470
FT /note= "Asn is N-glycosylated"
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FT Modified-site 488
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 502
FT /note= "Casein kinase II site"
FT Inhibitory-site 542. .722
FT Modified-site 576
FT /note= "Casein kinase II site"
FT Peptide 623. .640
FT /note= "used as immunogen to generate antibody AS 472"
FT Modified-site 626
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 694. .696
FT /note= "Asn is N-glycosylated"

FT Modified-site 715
FT /note= "Casein kinase II site"
FT Peptide 762. .1163
FT /note= "used as immunogen to generate antibody AS Bruna"
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FT /note= "Protein kinase C (PKC) site"
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FT /note= "Protein kinase C (PKC) site"
FT Modified-site 850
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FT Modified-site 855
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 863
FT /note= "Casein kinase II site"
FT Modified-site 868
FT /note= "Protein kinase C (PKC) site"
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FT /note= "Asn is N-glycosylated"
FT Modified-site 954
FT /note= "PKC and casein kinase II sites"
FT Modified-site 956
FT /note= "PKC and casein kinase II sites"
FT Region 975. .1162
FT /note= "This region is not essential for inhibitory activity"
FT Region 976. .1163
FT /note= "C-terminal common region found in Nogo A, B and C isoforms"
FT Domain 988. .1023
FT /label= Transmembrane_domain
FT /note= "C-terminal hydrophobic region specifically described in claim 16"
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FT /note= "Protein kinase C (PKC) site"
FT Modified-site 1071. .1073
FT /note= "Asn is N-glycosylated"
FT Modified-site 1073
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 1089
FT /note= "Protein kinase C (PKC) site"
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FT /label= Transmembrane_domain
FT /note= "C-terminal hydrophobic region specifically described in claim 16"
FT Modified-site 1141. .1143
FT /note= "Asn is N-glycosylated"
FT Modified-site 1143
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XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX

PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
DR N-PSDB; AAD01173.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 3; Fig 2A; 122pp; English.
XX
CC The present sequence is a rat Nogo A protein which is a potent neural
CC cell growth inhibitor and is free of all central nervous system (CNS)
CC myelin material with which it is natively associated. The protein was
CC derived from a cDNA generated by fusing R018U37-3, R1-3U21 cDNAs isolated
CC from hexanucleotides-primed rat brain stem/spinal cord library, and Ol18
CC cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins
CC and fragments displaying neurite growth inhibitory activity are used in
CC the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendrogloma, menangioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: The present sequence
CC designated as SEQ ID NO: 2 is stated to be the same as the sequence shown
CC in Fig. 13 (see AAY71384) of the specification. However, this sequence
CC does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers
XX
SQ Sequence 1163 AA;

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Query Match           100.0%;  Score 925;  DB 3;  Length 1163;
Best Local Similarity 100.0%;  Pred. No. 4e-89;
Matches 189;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Y 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
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D 975 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1034

Y 61 IOKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
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Db 1035 IQKSDEGHFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAV 1094
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Db 1095 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154
Qy 181 IPGLKRKAD 189
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Db 1155 IPGLKRKAD 1163

RESULT 3
AAY71384
ID AAY71384 standard; protein; 1163 AA.
XX
AC AAY71384;
XX
DT 02-NOV-2000 (first entry)
XX
DE Alternative version of rat neurite growth inhibitor Nogo A.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Inhibitory-site 1. .171
FT /note= "Inhibits NIH 3T3 fibroblast spreading"
FT Modified-site 30
FT /note= "Casein kinase II site"
FT Region 31. .58
FT /note= "Acidic region"
FT Region 172. .259
FT /note= "This region is not essential for inhibitory
FT activity"
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FT Misc-difference 404
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FT Modified-site 468. .470
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FT /note= "Casein kinase II site"
FT Inhibitory-site 542. .722
FT Modified-site 576
FT /note= "Casein kinase II site"
FT Peptide 623. .640
FT /note= "used as immunogen to generate antibody AS 472"
FT Modified-site 626
FT /note= "Protein kinase C (PKC) site"
FT Misc-difference 661
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FT Modified-site 694. .696
FT /note= "Asn is N-glycosylated"
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FT Peptide 762. .1163
FT /note= "used as immunogen to generate antibody AS Bruna"
FT Modified-site 784
FT /note= "Protein kinase C (PKC) site"
FT Misc-difference 820
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FT /note= "Protein kinase C (PKC) site"
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FT /note= "Casein kinase II site"
FT Modified-site 868
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 893
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FT Modified-site 912. .914
FT /note= "Asn is N-glycosylated"
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FT /note= "Asn is N-glycosylated"
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FT /note= "PKC and casein kinase II sites"
FT Region 975. .1162
FT /note= "This region is not essential for inhibitory
FT activity"

FT Region 976. .1163
FT /note= "C-terminal common region found in Nogo A, B and C isoforms"
FT Domain 988. .1023
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FT Modified-site 1071. .1073
FT /note= "Asn is N-glycosylated"
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FT /note= "Protein kinase C (PKC) site"
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FT /note= "Protein kinase C (PKC) site"
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FT /label= Transmembrane_domain
FT /note= "C-terminal hydrophobic region"
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FT /note= "Asn is N-glycosylated"
FT Modified-site 1143
FT /note= "Protein kinase C (PKC) site"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 3; Fig 13; 122pp; English.
XX
CC The present sequence is an alternative version of rat Nogo A protein
CC which is a potent neural cell growth inhibitor and is free of all central
CC nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendrolioma, menangioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The

CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. Note: The present
CC sequence is an alternative version of the Nogo A sequence shown in Fig.
CC 2A (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ
CC ID NO: 29 in disclosure of the specification. However the specification
CC does not include sequences for these SEQ ID numbers
XX

SQ Sequence 1163 AA;

Query Match 100.0%; Score 925; DB 3; Length 1163;
Best Local Similarity 100.0%; Pred. No. 4e-89;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 975 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1034

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV 120
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Db 1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV 1094

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Db 1095 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154

Qy 181 IPGLKRKAD 189
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Db 1155 IPGLKRKAD 1163

RESULT 4

ABB81074

ID ABB81074 standard; protein; 1163 AA.

XX

AC ABB81074;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnery; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; rat; receptor.

XX

OS Rattus norvegicus.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.
PR 19-MAY-1999; 99US-00314161.

xx

PA (YEDA) YEDA RES & DEV CO LTD.

xx

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;

xx

DR WPI; 2002-607255/65.

DR N-PSDB; ABN86600.

xx

PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.

xx

PS Example 5; Page 44-47; 93pp; English.

xx

The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific activated T cells, NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not an autoimmune disease or neoplasm. The disease results in a degenerative process occurring in either gray or white matter or both. The disease is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral disc herniation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral neuropathies associated with various diseases, including but not limited to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gammopathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangiectasia, Friedreich's ataxia, amyloid polyneuropathies, adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the rat neurotransmitter receptor protein Nogo-A, an example of NS-specific antigen

xx

SG Sequence 1163 AA:

Query Match 100.0%; Score 925; DB 5; Length 1163;

Best Local Similarity 100.0%: Pred. No 4e-89:

Matched 189: Conservative 0: Mismatches 0: Indols 0 0 0

QV

1 SVVDILLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60

Db 975 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 1034
Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKEELRRFLVDDLVDSLKFAV 120
Db 1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKEELRRFLVDDLVDSLKFAV 1094
Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
Db 1095 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154
Qy 181 IPGLKRKAD 189
Db 1155 IPGLKRKAD 1163

RESULT 5

ADB85283

ID ADB85283 standard; protein; 379 AA.

XX

AC ADB85283;

XX

DT 04-DEC-2003 (first entry)

XX

DE Rat foocen-m2 reticulon SEQ ID NO:164.

XX

KW rat; streptozocin; kinase; phosphatase; ion channel protein; receptor; transporter; G-protein coupled receptor; GPCR; DNA-binding proteins; protease; enzyme; analgesic; gene therapy; pain; diabetes.

XX

OS Rattus norvegicus.

XX

PN EP1284297-A2.

XX

PD 19-FEB-2003.

XX

PF 26-JUL-2002; 2002EP-00255228.

XX

PR 27-JUL-2001; 2001GB-00018354.

PR 07-FEB-2002; 2002GB-00002880.

XX

PA (WARN) WARNER LAMBERT CO.

XX

PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;

XX

DR WPI; 2003-364994/35.

DR N-PSDB; ADB85284.

XX

PT Use of gene sequence that is down-regulated in response to streptozocin-induced diabetes, vector, host cell, animal, polypeptide and antibody, in screening of compounds for treating or diagnosing pain.

XX

PS Disclosure; Page 239-240; 256pp; English.

XX

CC The invention relates to a novel isolated gene sequence that is down-regulated in the spinal cord in response to streptozocin-induced diabetes, or comprising, hybridising or having at least 80% sequence identity to a sequence whose expression products are kinases,

CC phosphatases, ion channel proteins, receptors, transporters, G-protein
CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,
CC given in the specification. A gene of the invention has analgesic
CC activity, and may have a use in gene therapy. The gene sequences, vector,
CC host cell, animal, polypeptide and antibody are useful for screening of
CC compounds for diagnosing or treating pain. The kits are useful for
CC simultaneous, separate or sequential detecting and/or quantifying down-
CC regulation of a gene sequence in the spinal cord of a mammal in response
CC to streptozocin-induced diabetes. The compound or pharmaceutical
CC composition is useful as a medicament for treating or diagnosing pain.
CC The present sequence represents a protein encoded by a gene of the
CC invention.

XX

SQ Sequence 379 AA;

Query Match 99.7%; Score 922; DB 7; Length 379;
Best Local Similarity 99.5%; Pred. No. 1.9e-89;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 191 AVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 250

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV 120
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 251 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV 310

Qy 121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
|||||||||||||||||||||||||||||||||||||||||||||||||
Db 311 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 370

Qy 181 IPGLKRKAD 189
|||||||||
Db 371 IPGLKRKAD 379

RESULT 6

ABB81077

ID ABB81077 standard; protein; 199 AA.

XX

AC ABB81077;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo-C.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnery; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; rat; receptor.

XX

OS Rattus norvegicus.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-00893348.
XX
PR 19-MAY-1998; 98IL-00124500.
PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.
PR 19-MAY-1999; 99US-00314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR N-PSDB; ABN86600.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.
XX
PS Example 5; Page 48-49; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents the rat
CC neurotransmitter receptor protein Nogo-C, an example of NS-specific
CC antigen
XX
SQ Sequence 199 AA;

Query Match 99.6%; Score 921; DB 5; Length 199;

Best Local Similarity 100.0%; Pred. No. 1.1e-89;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
 |||||||
 Db 12 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
 |||||||
 Db 72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 131

Qy 122 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
 |||||||
 Db 132 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 191

Qy 182 PGLKRKAD 189
 |||||
 Db 192 PGLKRKAD 199

RESULT 7
 AAY71383
 ID AAY71383 standard; protein; 360 AA.
 XX
 AC AAY71383;
 XX
 DT 02-NOV-2000 (first entry)
 XX
 DE Rat neurite growth inhibitor Nogo B.
 XX
 KW Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 1. .172
 FT /note= "Corresponds to amino acids 1-172 of Nogo A
 protein shown in AAY71310"
 FT Inhibitory-site 1. .171
 FT /note= "Inhibits NIH 3T3 fibroblast spreading"
 FT Modified-site 30
 FT /note= "Casein kinase II site"
 FT Region 31. .58
 FT /note= "Acidic region"
 FT Region 173. .360
 FT /note= "Corresponds to C-terminal 188 amino acids
 (residues 976-1163) of Nogo A protein (AAY71310). This
 region is common to Nogo A, B and C isoforms"
 FT Domain 185. .220
 FT /label= Transmembrane_domain
 FT /note= "C-terminal hydrophobic region"

FT Modified-site 221
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 268. .270
FT /note= "Asn is N-glycosylated"
FT Modified-site 270
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 286
FT /note= "Protein kinase C (PKC) site"
FT Domain 287. .322
FT /label= Transmembrane domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 338. .340
FT /note= "Asn is N-glycosylated"
FT Modified-site 340
FT /note= "Protein kinase C (PKC) site"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Example; Page; 122pp; English.
XX
CC The present sequence is a rat Nogo B protein which is a potent neural
CC cell growth inhibitor and is free of all central nervous system (CNS)
CC myelin material with which it is natively associated. The Nogo B
CC transcript arises as a result of alternative splicing of Nogo gene. Nogo
CC proteins and fragments displaying neurite growth inhibitory activity are
CC used in the treatment of neoplastic disease of the CNS e.g. glioma,
CC glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendrogloma, meningioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: The present sequence is
CC not given in the specification but is derived from Nogo A protein
CC sequence (AYY71310) and corresponds to residues 1-172 fused to 976-1163

CC of Nogo A. The specification claims an alternative version of this
CC sequence (see AAY71385.) which corresponds to residues 1-172 fused to 975
CC -1163 of Nogo A. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID
CC NO: 29 in disclosure of the specification. However the specification does
CC not include sequences for these SEQ ID numbers
XX
SQ Sequence 360 AA;

Query Match 99.6%; Score 921; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
Db 173 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 232
Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 121
Db 233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 292
Qy 122 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
Db 293 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 352
Qy 182 PGLKRKAD 189
Db 353 PGLKRKAD 360

RESULT 8
ABB81076
ID ABB81076 standard; protein; 360 AA.
XX
AC ABB81076;
XX
DT 05-NOV-2002 (first entry)
XX
DE Rat neurotransmitter receptor protein Nogo-B.
XX
KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnery; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; rat; receptor.
XX
OS Rattus norvegicus.
XX
PN US2002072493-A1.
XX
PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-00893348.
XX
PR 19-MAY-1998; 98IL-00124500.
PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

xx

PA (YEDA) YEDA RES & DEV CO LTD.

xx

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;

xx

DR WPI; 2002-607255/65.

DR N-PSDB; ABN86600.

xx

PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.

xx

PS Example 5; Page 47-48; 93pp; English.

xx

The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific activated T cells, NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not an autoimmune disease or neoplasm. The disease results in a degenerative process occurring in either gray or white matter or both. The disease is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral disc herniation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral neuropathies associated with various diseases, including but not limited to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangiectasia, Friedreich's ataxia, amyloid polyneuropathies, adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the rat neurotransmitter receptor protein Nogo-B, an example of NS-specific antigen

xx

Sequence 360 AA;

Query Match 99.6%; Score 921; DB 5; Length 360;

Best Local Similarity 100.0%; Pred. No. 2.3e-89;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61

Db

173 VVDLLYWRDIKKTGVVFGASLFLLLSLTIVFSIVSVTAYIALALLSVTISFRUYKGVIOAI 232

Qy	62	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE L RRFLVDDLVD SL KFAVL	121
Db	233	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE L RRFLVDDLVD SL KFAVL	292
Qy	122	MWVFTYVGALFNG L LL L ALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKI Q AKI	181
Db	293	MWVFTYVGALFNG L LL L ALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKI Q AKI	352
Qy	182	PGLKRKAD	189
Db	353	PGLKRKAD	360

RESULT 9

AAY71312

ID AAY71312 standard; protein; 522 AA.

XX

AC AAY71312;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo C.

XX

KW Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Region 1. .39

FT /note= "Sequence upstream to the N-terminus of Nogo C
 protein"

FT Misc-difference 3

FT /note= "Encoded by TAG"

FT Region 11. .191

FT /note= "Region specifically described in claim 16"

FT Misc-difference 29

FT /note= "Encoded by TAA"

FT Protein 40. .238

FT /label= Nogo_C_protein

FT Region 51. .238

FT /note= "C-terminal common region found in Nogo A, B and C
 isoforms "

FT Region 239. .522

FT /note= "Sequence downstream to the C-terminus of Nogo C
 protein"

FT Misc-difference 239

FT /note= "Encoded by TGA"

FT Misc-difference 263

FT /note= "Encoded by TGA"

FT Misc-difference 276

FT /note= "Encoded by TAG"

FT Misc-difference 281
FT /note= "Encoded by TGA"
FT Misc-difference 295
FT /note= "Encoded by TAA"
FT Misc-difference 298
FT /note= "Encoded by TAA"
FT Misc-difference 314
FT /note= "Encoded by TGA"
FT Misc-difference 318
FT /note= "Encoded by TGA"
FT Misc-difference 335
FT /note= "Encoded by TAG"
FT Misc-difference 371
FT /note= "Encoded by TGA"
FT Misc-difference 374
FT /note= "Encoded by TAG"
FT Misc-difference 380
FT /note= "Encoded by TAA"
FT Misc-difference 406
FT /note= "Encoded by TAA"
FT Misc-difference 408
FT /note= "Encoded by TAG"
FT Misc-difference 410
FT /note= "Encoded by TAA"
FT Misc-difference 422
FT /note= "Encoded by TAA"
FT Misc-difference 433
FT /note= "Encoded by TGA"
FT Misc-difference 440
FT /note= "Encoded by TAG"
FT Misc-difference 453
FT /note= "Encoded by TAG"
FT Misc-difference 465
FT /note= "Encoded by TAG"
FT Misc-difference 482
FT /note= "Encoded by TAG"
FT Misc-difference 513
FT /note= "Encoded by TAA"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
DR N-PSDB; AAD01175.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.

xx

PS Claim 7; Fig 14; 122pp; English.

xx

CC The present sequence is a rat Nogo C protein which is a potent neural
CC cell growth inhibitor and is free of all central nervous system (CNS)
CC myelin material with which it is natively associated. Nogo proteins and
CC fragments displaying neurite growth inhibitory activity are used in the
CC treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendrolioma, menangioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However the specification does not include sequences for
CC these SEQ ID numbers

xx

SQ Sequence 522 AA;

RESULT 10

AAV71559

ID AAY71559 standard; protein; 199 AA.

xx

AC AAY71559;

xx

DT 02-NOV-2000 (first entry)

xx

DE Rat Nogo C/Nogo A proteins derived fragment to construct mutant Nogo-C.

XX

KW Rat; neurite growth inhibitor; Nogo A; Nogo C; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; menangioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.

XX

OS *Rattus* sp.

XX

FH Key Location/Qualifiers
FT Region 1. .11
FT /note= "Corresponds to residues 40-50 of rat Nogo C
FT protein shown in AAY71312"
FT Region 12. .199
FT /note= "Corresponds to residues 975-1162 of rat Nogo A
FT protein shown in AAY71310"

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US026160.

XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.

XX

PS Example; Page; 122pp; English.

XX

CC The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendrogloma, menangioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is derived by fusing two fragments from rat Nogo C and Nogo A proteins.

CC The fragment is used in the construction of mutant Nogo-C which is
CC composed of His-tag/T7-tag/Nogo-C N-terminus (11 aa) + Nogo-A sequence aa
CC 975-1162. Nogo A deletion mutants were used for mapping the inhibitory
CC sites of Nogo protein. Major inhibitory region was identified in the Nogo
CC A sequence from amino acids 172-974, particularly amino acids 542-722. In
CC addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
CC fibroblast spreading. Note: The present sequence is not given in the
CC specification but is derived from rat Nogo C sequence shown in AAY71312
CC and Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers

XX

SQ Sequence 199 AA;

Query Match 99.4%; Score 919; DB 3; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 12 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 71

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 72 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 131

Qy 121 LMWVFTYVGALFNGLTLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 132 LMWVFTYVGALFNGLTLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 191

Qy 181 IPGLKRKA 188

||| |||

Db 192 IPGLKRKA 199

RESULT 11

AAY71558

ID AAY71558 standard; protein; 359 AA.

XX

AC AAY71558;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat Nogo A protein fragment used in the construction of mutant Nogo-B.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Region 1. .171
FT /note= "Corresponds to residues 1-171 of rat Nogo A
FT protein shown in AAY71310"
FT Region 172. .359
FT /note= "Corresponds to residues 975-1162 of rat Nogo A
FT protein shown in AAY71310"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Example; Page; 122pp; English.
XX
CC The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendrolioma, menangioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is derived by fusing two fragments of rat Nogo A protein shown in
CC AAY71310. The fragment is used in the construction of mutant Nogo-B. The
CC mutant is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-171 +
CC 975-1162. Nogo A deletion mutants were used for mapping the inhibitory
CC sites of Nogo protein. Major inhibitory region was identified in the Nogo
CC A sequence from amino acids 172-974, particularly amino acids 542-722. In
CC addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
CC fibroblast spreading. Note: The present sequence is not given in the
CC specification but is derived from rat Nogo A sequence shown in AAY71310.
CC SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in
CC disclosure of the specification. However, the specification does not
CC include sequences for these SEQ ID numbers
XX

SQ Sequence 359 AA;

RESULT 12

AAY71563

ID AAY71563 standard; protein; 403 AA.

xx

AC AAY71563;

xx

DT 02-NOV-2000 (first entry)

xx

DE Rat Nogo A protein fragment used in the construction of mutant EST.

xx

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnos;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.

xx

OS Rattus sp.

xx

PN WO200031235-A2.

XX

PD 02-JUN-2000.

25

PF 05-NOV-1999; 99W0-US026160.

88

PR 06-NOV-1998; 980S-0107446P.
XX

八

PA (SCHW) SCHWAB H E.
PA (CHEN/) CHEN M S

XX (CHEN) CHEN H. S.

PT

XX SORVAB FILE, SORVAB FILE,

DR

xx

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.

xx

PS Example; Page; 122pp; English.

xx

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendrogloma, menangioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a fragment of rat Nogo A protein shown in AAY71310, which is used in the construction of mutant EST. The mutant is composed of His-tag/T7-tag/Nogo-A sequence aa 760-1162. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers

xx

SQ Sequence 403 AA;

Query Match 99.4%; Score 919; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 4.4e-89;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60

Db 216 SVVDLLYWRDIKKTGVVFGASLFLLLS廖TVFSIVSVTAYIALALLSVTISFRIYKGVIQA 275

QY 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
|||||

Db 276 I Q K S D E G H P F R A Y L E S E V A I S E E L V Q K Y S N S A L G H V N S T I K E L R R L F L V D D L V D S L K F A V 335

DB 336 LMWVFTYVGALFNGLTLILALISLFSIPVVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 395

Qy 181 IPGLKRKA 188

2007 EDITION

DB 396 TPGLKRKA 403

RESULT 13
AA71557
ID AAY71557 standard; protein; 1162 AA.
XX
AC AAY71557;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.
XX
OS Rattus sp.
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Example; Page; 122pp; English.
XX
CC The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendrogloma, menangioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can

CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is a truncated form of rat Nogo A protein shown in AAY71310, which is
CC used in the construction of mutant Nogo-A. Nogo-A is composed of His-
CC tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were
CC used for mapping the inhibitory sites of Nogo protein. Major inhibitory
CC region was identified in the Nogo A sequence from amino acids 172-974,
CC particularly amino acids 542-722. In addition, N-terminal region 1-171
CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC present sequence is not given in the specification but is derived from
CC rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers

XX

SQ Sequence 1162 AA;

Query Match 99.4%; Score 919; DB 3; Length 1162;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
| |||||||
Db 975 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1034
| |||||||
Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSDLKFAV 120
| |||||||
Db 1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSDLKFAV 1094
| |||||||
Qy 121 LMWVFTYVGALFNGLTLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
| |||||||
Db 1095 LMWVFTYVGALFNGLTLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154
| |||||||
Qy 181 IPGLKRKA 188
| |||||
Db 1155 IPGLKRKA 1162

RESULT 14

AAY95012

ID AAY95012 standard; protein; 893 AA.

XX

AC AAY95012;

XX

DT 19-JUN-2000 (first entry)

XX

DE Human secreted protein vb22_1, SEQ ID NO:64.

XX

KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive.

XX

OS Homo sapiens.

XX

PN WO200011015-A1.

XX

PD 02-MAR-2000.

XX
PF 24-AUG-1999; 99WO-US019351.
XX
PR 24-AUG-1998; 98US-0097638P.
PR 24-AUG-1998; 98US-0097659P.
PR 09-SEP-1998; 98US-0099618P.
PR 28-SEP-1998; 98US-0102092P.
PR 25-NOV-1998; 98US-0109978P.
PR 23-DEC-1998; 98US-0113645P.
PR 23-DEC-1998; 98US-0113646P.
PR 23-AUG-1999; 99US-00379246.
XX
PA (ALPH-) ALPHAGENE INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-224657/19.
XX
PT New secreted or transmembrane proteins and polynucleotides encoding them,
PT useful for treating neurodegenerative disorders, autoimmune diseases and
PT cancer.
XX
PS Claim 73; Page 322-325; 357pp; English.
XX
CC The invention relates to 40 human secreted proteins (AAV94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins
CC of the invention include those that are thought to be only partially
CC secreted, i.e., transmembrane proteins. The proteins of the invention may
CC exhibit one or more activities selected from the following: cytokine
CC activity; cell proliferation; differentiation; immune modulation;
CC haematopoiesis regulation; tissue growth activity; activin/inhibin
CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC activity; anti-inflammatory activity; and tumour inhibition activity. The
CC proteins may be administered to patients as vaccines, and the nucleotides
CC may be used as part of a gene therapy regime. Diseases or conditions that
CC may be treated using the proteins or nucleotides of the invention include
CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular
CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;
CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;
CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and
CC allergic reactions such as asthma and anaemia. They may also be used for
CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal
CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease
CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin
CC activity may additionally be useful as contraceptives. Nucleic acid
CC sequences of the invention may be used in chromosome mapping, and as a
CC source of diagnostic primers and probes. The present sequence represents
CC one of the 40 proteins of the invention
XX
SQ Sequence 893 AA;

Query Match 98.2%; Score 908; DB 3; Length 893;
Best Local Similarity 97.4%; Pred. No. 1.8e-87;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVFGASLFLLSLTVFSIVSVTAYIALALLSVTI SFRIYKGVIQA 60

Db 705 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 764
Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
Db 765 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 824
Qy 121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
Db 825 LMWVFTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 884
Qy 181 IPGLKRKAD 189
Db 885 IPGLKRKAE 893

RESULT 15

ABU11573

ID ABU11573 standard; protein; 983 AA.

XX

AC ABU11573;

XX

DT 12-FEB-2003 (first entry)

XX

DE Human MDDT polypeptide SEQ ID 520.

XX

KW MDDT; human; disease detection and treatment molecule polypeptide;
KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW gene therapy; protein replacement therapy; cell proliferative disorder;
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopenia;
KW psoriasis; hepatitis.

XX

OS Homo sapiens.

XX

PN WO200279449-A2.

XX

PD 10-OCT-2002.

XX

PF 27-MAR-2002; 2002WO-US009944.

XX

PR 28-MAR-2001; 2001US-0279619P.

PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.

PR 17-MAY-2001; 2001US-0291849P.

PR 19-JUN-2001; 2001US-0299428P.

PR 20-JUN-2001; 2001US-0299776P.

PR 20-JUN-2001; 2001US-0300001P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;

PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstein EH;

PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-058431/05.
DR N-PSDB; ABX34563.
XX
PT New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis.
XX
PS Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.
XX
CC This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded
CC by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences
XX
SQ Sequence 983 AA;

```

Query Match          98.2%;  Score 908;  DB 6;  Length 983;
Best Local Similarity 97.4%;  Pred. No. 2.1e-87;
Matches 184;  Conservative 3;  Mismatches 2;  Indels 0;  Gaps 0;

Y      1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
D      795 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 854

Y      61 I QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV 120
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
D      855 I QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSDLKFAV 914

Y      121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
D      915 LMWVFTYVGALFNGLTLILALISLFSVPVIYERHQAOQIDHYLGLANKNVKDAMAKIQAK 974

Y      181 I PGLKRKAD 189
|:|||||:|
D      975 I PGLKRKAE 983

```

Search completed: September 29, 2004, 18:13:55
Job time : 17.5871 secs

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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:09:33 ; Search time 4.69196 Seconds
(without alignments)
2079.581 Million cell updates/sec

Title: US-09-830-972-2_COPY_975_1163
Perfect score: 925
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PECTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	904	97.7	199	2	US-08-700-607-1	Sequence 1, Appli
2	679	73.4	208	2	US-08-700-607-7	Sequence 7, Appli
3	679	73.4	356	2	US-08-700-607-6	Sequence 6, Appli
4	679	73.4	776	2	US-08-700-607-5	Sequence 5, Appli
5	665	71.9	267	2	US-08-700-607-8	Sequence 8, Appli
6	539.5	58.3	168	4	US-09-149-476-563	Sequence 563, App
7	516	55.8	241	2	US-08-700-607-3	Sequence 3, Appli
8	286	30.9	92	4	US-09-149-476-411	Sequence 411, App
9	100	10.8	80	3	US-08-905-223-411	Sequence 411, App
10	95	10.3	468	4	US-08-487-596-8	Sequence 8, Appli
11	95	10.3	468	4	US-08-660-451A-8	Sequence 8, Appli

12	88.5	9.6	1278	4	US-09-462-136-2	Sequence 2, Appli
13	86.5	9.4	592	4	US-09-134-000C-5477	Sequence 5477, Ap
14	86	9.3	414	4	US-08-956-171E-5246	Sequence 5246, Ap
15	85.5	9.2	1051	4	US-09-134-001C-5005	Sequence 5005, Ap
16	84.5	9.1	593	4	US-09-328-352-4866	Sequence 4866, Ap
17	82	8.9	614	4	US-09-540-236-2858	Sequence 2858, Ap
18	81.5	8.8	280	4	US-09-543-681A-6175	Sequence 6175, Ap
19	81	8.8	744	4	US-09-785-381-1	Sequence 1, Appli
20	81	8.8	744	4	US-09-785-381-3	Sequence 3, Appli
21	80.5	8.7	598	2	US-08-853-659A-53	Sequence 53, Appl
22	79	8.5	289	4	US-09-540-236-2019	Sequence 2019, Ap
23	79	8.5	554	4	US-09-252-991A-27968	Sequence 27968, A
24	78.5	8.5	748	3	US-09-061-764A-19	Sequence 19, Appl
25	78	8.4	231	4	US-09-198-452A-419	Sequence 419, App
26	78	8.4	420	4	US-09-134-001C-3805	Sequence 3805, Ap
27	78	8.4	424	4	US-09-543-681A-7510	Sequence 7510, Ap
28	78	8.4	970	4	US-09-795-927-7	Sequence 7, Appli
29	78	8.4	1053	4	US-09-328-352-5058	Sequence 5058, Ap
30	77.5	8.4	492	4	US-09-134-000C-4808	Sequence 4808, Ap
31	77	8.3	154	1	US-08-366-783-5	Sequence 5, Appli
32	77	8.3	292	4	US-09-489-039A-12212	Sequence 12212, A
33	77	8.3	720	4	US-09-134-000C-5631	Sequence 5631, Ap
34	76.5	8.3	601	4	US-09-134-000C-5783	Sequence 5783, Ap
35	76	8.2	700	4	US-09-543-681A-4969	Sequence 4969, Ap
36	76	8.2	993	4	US-08-836-687B-30	Sequence 30, Appl
37	75.5	8.2	231	4	US-09-724-623-116	Sequence 116, App
38	75.5	8.2	408	4	US-09-107-532A-6198	Sequence 6198, Ap
39	75.5	8.2	444	4	US-09-543-681A-5355	Sequence 5355, Ap
40	75.5	8.2	454	4	US-09-904-615-165	Sequence 165, App
41	75.5	8.2	501	4	US-09-328-352-5227	Sequence 5227, Ap
42	75.5	8.2	613	4	US-09-107-532A-6935	Sequence 6935, Ap
43	75	8.1	871	4	US-09-255-829-2	Sequence 2, Appli
44	75	8.1	871	4	US-09-255-829-8	Sequence 8, Appli
45	75	8.1	871	4	US-09-255-829-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1
 US-08-700-607-1
; Sequence 1, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-700-607-1

RESULT 2
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307311

US-08-700-607-7

Query Match 73.4%; Score 679; DB 2; Length 208;
Best Local Similarity 67.9%; Pred. No. 7.5e-65;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

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QY	63	KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAVLM	122
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Db	82	KTDEGHPFKAYLEITLSQEIQKYTDCLQFYVNSTLKELRRFLVQDLVDLSLKFAVLM	141
QY	123	WVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP	182
		: : : : : : : :	
Db	142	WLLTYVGALFNGLTLMAVVSMAFTLPVYYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP	201
QY	183	GLKRKAD 189	
		:	
Db	202	GAKRHAE 208	

RESULT 3
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
US-08-700-607-6

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Query Match           73.4%;  Score 679;  DB 2;  Length 356;
Best Local Similarity 67.9%;  Pred. No. 1.6e-64;
Matches 127;  Conservative 31;  Mismatches 29;  Indels 0;  Gaps 0;

Qy      3 VDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
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Db      170 IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 229

Qy      63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
        |:||||||:||| | : :||: :|||:: :|||:||||||| ||||||||| |
Db      230 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 289

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Qy 123 WVFTYVGALFNGLTLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
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Db 290 WLLTYVGALFNGLTLMAVVSMTLPVYVVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 349
| || |:
Qy 183 GLKRKAD 189
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Db 350 GAKRHAE 356

RESULT 4

US-08-700-607-5

; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307

US-08-700-607-5

Query Match 73.4%; Score 679; DB 2; Length 776;
Best Local Similarity 67.9%; Pred. No. 4.6e-64;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

Qy 3 VDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
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Db 590 IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQ 649

Qy 63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAVLM 122
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Db 650 KTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELELRRLFLVQDLVDSLKFAVLM 709

Qy 123 WVFTYVGALFNGLTLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
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Db 710 WLLTYVGALFNGLTLLMAVVSMSFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 769

Qy 183 GLKRKAD 189
| || |:
Db 770 GAKRHAE 776

RESULT 5

US-08-700-607-8

; Sequence 8, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 281046
US-08-700-607-8

Query Match 71.9%; Score 665; DB 2; Length 267;
Best Local Similarity 67.2%; Pred. No. 3.3e-63;
Matches 123; Conservative 32; Mismatches 28; Indels 0; Gaps 0;

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Db 13 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQ 72

Qy 63 KSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAVLM 122
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Db 73 KTDEGHPPFKAYLELEITLSQEIQKYTDCLQLYVNSTLKELRRLFLVQDLVDSLKFAVLM 132

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Qy 183 GLK 185
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Db 193 GAR 195

RESULT 6

US-09-149-476-563

;
; Sequence 563, Application US/09149476
;
; Patent No. 6420526
;
; GENERAL INFORMATION:
;
; APPLICANT: Rosen et al.
;
; TITLE OF INVENTION: 186 Human Secreted proteins
;
; FILE REFERENCE: PZ002P1
;
; CURRENT APPLICATION NUMBER: US/09/149,476
;
; CURRENT FILING DATE: 1998-09-08
;
; EARLIER APPLICATION NUMBER: PCT/US98/04493
;
; EARLIER FILING DATE: 1998-03-06
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; EARLIER APPLICATION NUMBER: 60/040,162
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; EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/047,615
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; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/056,886
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; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060

; EARLIER FILING DATE: 1997-10-02

Query Match 58.3%; Score 539.5; DB 4; Length 168;
Best Local Similarity 59.3%; Pred. No. 4.8e-50;
Matches 99; Conservative 36; Mismatches 31; Indels 1; Gaps 1;

Qy 24 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLEVAISEE 83
:|||| ||::|| :|: |||||||||||| ||||:|||:||||:|||: :: :|
Db 1 MLLSLAAFSVISVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSE 60

Qy 84 LVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLALI 143
| |::| :|: | :|: |||||:|||||| | | |:| |||:|||:|||:|||:
Db 61 AFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAVFMWLMTYVGAVFNGITLLILAE 120

Qy 144 SLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGL-KRKAD 189
:||:||:||::: |||||:||| | : |||||:|||: |||:
Db 121 LIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKAE 167

RESULT 7

US-08-700-607-3

; Sequence 3, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,607

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 241 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: THP1NOB01
; CLONE: 31870
US-08-700-607-3

Query Match 55.8%; Score 516; DB 2; Length 241;
Best Local Similarity 59.9%; Pred. No. 2.6e-47;
Matches 94; Conservative 33; Mismatches 30; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60
 :| ||: ||||:|||| ||| :| :|||| ||::|| :|: ||||||||||||| |||||
Db 47 AVHDLIXWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLLALLSVTISFRIYKSVIQA 106

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV 120
 :||||:|||||:|||: :: :| | | |: ||| :| : |||||:||||||| |||
Db 107 VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAV 166

Qy 121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQV 157
 ||: |||||:|||:|||||| : : ||::| ::|||
Db 167 FMWLMTYVGAVFNGITLLILAEELLIIXSVPIVYXKYKV 203

RESULT 8

US-09-149-476-411

; Sequence 411, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 30.9%; Score 286; DB 4; Length 92;

Best Local Similarity 56.0%; Pred. No. 2.9e-23;
Matches 51; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

Qy 90 NSALGHVNSTIKELRRLFLVDDLVDLSKFAVLMWVFTYVGALFNGLTLLILALISLFSIP 149
|:|: |:| :| : |||||:||||||| ||| :| |||||:|||:||||| :|:|:
Db 2 NAAMVHINRALKLIIIRLFLVEDLVDSLKLAVFMWLMTYVGAVFNGITLLILAELLIFSVP 61

Qy 150 VIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
::|:|::: |||||:|:| | :|| :|
Db 62 IVYEKYKTQIDHYVGIARDQTKSIVEKIPSK 92

RESULT 9

US-08-905-223-411

; Sequence 411, Application US/08905223

; Patent No. 6222029

; GENERAL INFORMATION:

; APPLICANT: Edwards, Jean-Baptiste D.

; APPLICANT: Duelert, Aymeric

; APPLICANT: Lacroix, Bruno

; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS

; NUMBER OF SEQUENCES: 503

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 501 West Broadway

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-3505

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Win95

; SOFTWARE: Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/905,223

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Israelsen, Ned A.

; REGISTRATION NUMBER: 29,655

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 235-8550

; TELEFAX: (619) 235-0176

; INFORMATION FOR SEQ ID NO: 411:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 80 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN

; ORIGINAL SOURCE:

; ORGANISM: Homo Sapiens

; TISSUE TYPE: Brain

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: -78..-1

; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 6.3
; OTHER INFORMATION: seq TLIMLLSWQLSVS/SV
US-08-905-223-411

Query Match 10.8%; Score 100; DB 3; Length 80;
Best Local Similarity 57.1%; Pred. No. 0.002;
Matches 20; Conservative 8; Mismatches 5; Indels 2; Gaps 1;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLS--LTVFSI 33
:| ||::||||:|||| ||| :| :||| ||| :| :| :|:
Db 46 AVHDLIFWRDVKKTGFVFGTTLIMLLSWQLSVSSV 80

RESULT 10

US-08-487-596-8

; Sequence 8, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990

; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-596-8

Query Match 10.3%; Score 95; DB 4; Length 468;
Best Local Similarity 21.5%; Pred. No. 0.078;
Matches 41; Conservative 33; Mismatches 61; Indels 56; Gaps 7;

Qy 24 LLLSLTVFSIV-----SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP- 69
Db 288 VLVSLTVFLLVIEEIPSSSKVIPPLIGEYLVFTMIFVTL SIMVTFAINIHRRSSTHNA 347
Qy 70 -----FRAYLESEVAISEELVQ---KYSNSALGHVNSTIKELRRLF 107
Db 348 MAPLVRKIFLHTLPKLLCMRSHVDRYFTQKEETESGGSPKSSRNTLEAALNSIRYITRHI 407
Qy 108 L---VDDLVDSLKF-----AVLMWVFTYVGALFNGLTLLALISLFSIPVIYERHQV 157
Db 408 MKENDVREVVEDWKFIAQVLDRMFLWTFLFVS-----IVGSLGLF-VPVIYKWANI 457
Qy 158 QIDHYLGLANK 168
Db 458 LIPVHIGNANK 468

RESULT 11

US-08-660-451A-8

; Sequence 8, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 06/07/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-660-451A-8

Query Match 10.3%; Score 95; DB 4; Length 468;
Best Local Similarity 21.5%; Pred. No. 0.078;
Matches 41; Conservative 33; Mismatches 61; Indels 56; Gaps 7;

Qy 24 LLLSLTVFSIV-----SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP- 69
Db 288 VLVSLTVFLLVIEEIIPSSSKVPIPLIGEYLVFTMIFVTLSIMVTVFAINIHRSSSTHNA 347

Qy 70 -----FRAYLESEVAISEELVQ---KYSNSALGHVNSTIKELRRLF 107
Db 348 MAPLVRKIFLHTLPKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHI 407

Qy 108 L---VDDLVDSLKF----AVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQV 157
Db 408 MKENDVREVVEDWKFIAQVLDRMFLWTFLFVS-----IVGSLGLF-VPVIYKWANI 457

Qy 158 QIDHYLGLANK 168
Db 458 LIPVHIGNANK 468

RESULT 12
US-09-462-136-2
; Sequence 2, Application US/09462136
; Patent No. 6426198
; GENERAL INFORMATION:
; APPLICANT: Carstea, et al.
; TITLE OF INVENTION: Genes for Niemann-Pick Type C Disease

; FILE REFERENCE: 4239-53894
; CURRENT APPLICATION NUMBER: US/09/462,136
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/US98/13862
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/051,682
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-136-2

Query Match 9.6%; Score 88.5; DB 4; Length 1278;
Best Local Similarity 25.7%; Pred. No. 1.6;
Matches 39; Conservative 25; Mismatches 51; Indels 37; Gaps 7;

Qy 46 SVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR 105
::||| : : : : | || :: | : ||| || ||
Db 598 NLTISFTAERSIEDELNRESDDSDV-----TVVISYAIMFLYISLALGH---IKSCRR 647

Qy 106 LFLVDD-----LVDSLKFAVLMWVFTYVGALFNGLTLLILALI-----SLF 146
| ||| |: | : ||:| | |||::: :| ::|
Db 648 L-LVDSKVSLGIAGILIVLSSVACSLGVFSYIGL---PLTLIVIEVIPFLVLAVGVDNIF 703

Qy 147 SIPVIYERHQ---VQIDHYLGLANKSVKDAM 174
: |:| : | :| || | :|
Db 704 ILVQAYQRDERLQGETLDQQLGRVLGEVAPSM 735

RESULT 13
US-09-134-000C-5477
; Sequence 5477, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5477
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5477

Query Match 9.4%; Score 86.5; DB 4; Length 592;
Best Local Similarity 20.9%; Pred. No. 0.88;
Matches 49; Conservative 41; Mismatches 61; Indels 83; Gaps 12;

Qy 7 YWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFR-----IYK 55
:|: :|: || :| : ||::| : ||: :| : :|:
Db 45 FWKTVKR-----LFRYMSKRLSIIAV---LVLIAAAVVFQIQTPKVLGQATTEIFK 93

Qy 56 GVIQAIQKSDEGHPFRA-----YLESEV-----A 79
||:: : :| : || || |
Db 94 GVMKGAAEMKQGLKITSFPIDFDKIGQILLIVIAMYLISAVNFLQQVIMTRVSQRTVYE 153

Qy 80 ISEELVQKYSNSALG---HVNSTIKELRRLFLVDDLVDSLK---FAVLMWVFTYVGALF 132
:|| | : : || | | | : :||: :|| : :|:
Db 154 LRQELEAKMNKVPISYYDIHSNGDIMS-RAINMDNIASTLQQNLTQLITSIVTFVGVLW 212

Qy 133 NGLT---LLILAL---ISLFSIPVIYERHQVQIDHY---LGLANKSVKD 172
|| | :|| :|| :|: || | | |: || | | |::
Db 213 MMLTISWQLTLIALATVPLSLIVVMVVAPRSQ---KHFAAQKSLGLLNNQVEE 263

RESULT 14

US-08-956-171E-5246

; Sequence 5246, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5246:
US-08-956-171E-5246

Query Match 9.3%; Score 86; DB 4; Length 414;
Best Local Similarity 22.2%; Pred. No. 0.61;
Matches 42; Conservative 37; Mismatches 78; Indels 32; Gaps 7;

Qy 2 VVDLLYWRDIKKTGV-VFGASLFLLLSLTVFSIVSVTAYI-ALALLSVTISFRIYKGVIQ 59
Db 3 IVILLFLRNIRTTAISIISIPLSLLMALIALKLSDVSLNILTGLTVAIG-RVIDDSIV 61

Qy 60 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFA 119
Db 62 VVE-----NIYRRLTDSEEQLKGENL-----IISATTEVFKPIMSSTLVTIIVFL 106

Qy 120 VLMWVFTYVGALFN-----GLTLLLALISLFSIPVI-----YERHQVQIDHYLGL 165
Db 107 PLVFVSGSVGEMFRPFALAIAFSLLASLLVSITLVPALAATLFKKGVKRRNKQHQEGLGV 166

Qy 166 ANKSVKDAM 174
Db 167 VSTTYKKVL 175

RESULT 15
US-09-134-001C-5005
; Sequence 5005, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5005
; LENGTH: 1051
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5005

Query Match 9.2%; Score 85.5; DB 4; Length 1051;
Best Local Similarity 22.1%; Pred. No. 2.5;

Matches 43; Conservative 39; Mismatches 62; Indels 51; Gaps 9;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSV-----TAYIALALLSVTISFRIYKG 56
:|| ||: |::|: | : ||||: | ||| | :|:::
Db 380 IVILLFLRNIRTTAI-----SIVSIPMSILIALALKLSNVSLNILTTLGA 424

Qy 57 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYS--NSALGHVNSTIKELRRLF--LVDD 111
: || : :: : | : :: | | | | | | | :| :
Db 425 LTVAIGR-----VIDDSIVVVENIFRRLSDPNEKLKGENLIISATREVFKPIMSST 475

Qy 112 LVDSLKFAVLMWVFTYVGALFN---GLTLLLILA--LISLFSIPVI--YERHQVQIDHY 162
|| : | |::| | | :| :| :|| | :|: | :| : : ::
Db 476 LVTIVVFLPLVFVSGSGEMFRPFALAITFSLLASLLVSITLVP SLGATFFKN----- 528

Qy 163 LGLANKSVKDAMAKI 177
|: |: |: : :
Db 529 -GVKNREQKEGLGTV 542

Search completed: September 29, 2004, 18:21:00
Job time : 6.69196 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:05:43 ; Search time 4.62587 Seconds
(without alignments)
3930.111 Million cell updates/sec

Title: US-09-830-972-2_COPY_975_1163
Perfect score: 925
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLRKAD 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	679	73.4	208	2	I60904	neuroendocrine-spe
2	679	73.4	776	2	A46583	neuroendocrine-spe
3	665	71.9	267	2	A60021	tropomyosin-relate
4	321	34.7	2484	2	T26216	hypothetical prote
5	321	34.7	2607	2	T26215	hypothetical prote
6	320	34.6	222	2	T26213	hypothetical prote
7	194	21.0	255	2	E84899	hypothetical prote
8	182	19.7	271	2	T13013	hypothetical prote
9	163	17.6	275	2	T05595	hypothetical prote
10	142	15.4	393	2	S67763	probable membrane
11	135.5	14.6	242	2	B85016	hypothetical prote
12	134	14.5	183	2	A84527	hypothetical prote
13	131.5	14.2	295	2	S59439	probable membrane

14	123	13.3	206	2	T01153	probable seed matu
15	109.5	11.8	264	2	T47948	hypothetical prote
16	107.5	11.6	203	2	T47571	hypothetical prote
17	94	10.2	288	2	B90043	conserved hypothet
18	93.5	10.1	457	2	H85095	hypothetical prote
19	92.5	10.0	458	2	A72258	hypothetical prote
20	92.5	10.0	677	2	F95232	immunity protein,
21	92.5	10.0	680	2	H98096	conserved hypothet
22	91	9.8	160	2	C84422	hypothetical prote
23	90.5	9.8	442	2	C75057	hypothetical prote
24	89	9.6	224	2	D71915	hydrogenase, cytoc
25	89	9.6	468	2	A38223	nicotinic acetylch
26	87	9.4	1065	2	E69795	acrilavin resista
27	86	9.3	589	2	F64201	transport ATP-bind
28	86	9.3	1055	2	H90023	hypothetical prote
29	85.5	9.2	296	2	S46018	probable membrane
30	85.5	9.2	299	2	B69155	hypothetical prote
31	85	9.2	299	2	C64397	hypothetical prote
32	85	9.2	459	2	G86264	F3F19 hypothetical
33	85	9.2	689	2	T09007	ABC-transporter ho
34	84.5	9.1	151	2	G96705	unknown protein, 7
35	83.5	9.0	445	2	AD2358	glucosyltransferas
36	83.5	9.0	570	2	S52765	secD protein - Str
37	83.5	9.0	823	2	H83724	hypothetical prote
38	83	9.0	180	2	E97200	probable phosphata
39	83	9.0	252	2	G97886	hypothetical prote
40	83	9.0	388	1	D70006	conserved hypothet
41	82.5	8.9	410	2	A95044	conserved hypothet
42	82.5	8.9	502	2	F70316	conserved hypothet
43	82.5	8.9	675	2	T50332	SCT1 homolog SPBC1
44	82.5	8.9	937	2	T41400	probable peroxisom
45	82	8.9	224	1	A64599	hydrogenase (EC 1.

ALIGNMENTS

RESULT 1

I60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: I60904

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

```

Query Match           73.4%;  Score 679;  DB 2;  Length 208;
Best Local Similarity 67.9%;  Pred. No. 2.5e-52;
Matches 127;  Conservative 31;  Mismatches 29;  Indels 0;  Gaps 0;

Y      3 VDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
Y      :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Y      22 IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQ 81

Y      63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAVLM 122
Y      |:||||||:|||| |: :||| :|||:: :||||:||||||| ||||||||| ||||||||| |
Y      82 KTDEGHPFKAYLELEITLSQEIQKYTDCIQLFYVNSTLKELRRLFLVQDLVDSDLKFAVLM 141

Y      123 WVFTYVGALFNGLTLLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
Y      |: |||||||:|||:||:||:||:||:||:|| :|| ||| ||| : :|||:||| |
Y      142 WLLTYVGALFNGLTLLMAVVSMFTLPVVYVKHQAQIDQYLGVRTHINAVVAKIQAKIP 201

Y      183 GLKRKAD 189
Y      | || |:
Y      202 GAKRHAE 208

```

RESULT 2

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: *Homo sapiens* (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13

A;Title: Cloning and expression of al-

neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A; Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 421-776 <ROE2>

A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309

C; Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 73.4%; Score 679; DB 2; Length 776;
 Best Local Similarity 67.9%; Pred. No. 1.2e-51;
 Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

Qy	3 VDLLYWRDIKKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ	62
	: : : : : : : :	
Db	590 IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ	649
Qy	63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFVAVLM	122
	: : : : : : : :	
Db	650 KTDEGHPFKAYLELEITLSQEIQKYTDCLQYVNSTLKELRRLFLVQDLVDSLKFVAVLM	709
Qy	123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP	182
	: :: : : : : :	
Db	710 WLLTYVGALFNGLTLLMAVVSMMFTLPVYYVKHQAQIDQYLGVRTHINAVVAKIQAKIP	769
Qy	183 GLKRKAD 189	
	:	
Db	770 GAKRHAE 776	

RESULT 3

A60021

tropomyosin-related protein, neuronal - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999

C;Accession: A60021

R;Wieczorek, D.F.; Hughes, S.R.

Brain Res. Mol. Brain Res. 10, 33-41, 1991

A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.

A;Reference number: A60021; MUID:91278684; PMID:1647480

A;Accession: A60021

A;Molecule type: mRNA

A;Residues: 1-267 <WIE>

A;Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550

C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropomyosin probe but does not show homology in amino acid sequence.

Query Match 71.9%; Score 665; DB 2; Length 267;
 Best Local Similarity 67.2%; Pred. No. 5.7e-51;
 Matches 123; Conservative 32; Mismatches 28; Indels 0; Gaps 0;

Qy	3 VDLLYWRDIKKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ	62
	: : : : : : : :	
Db	13 IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ	72

Qy	63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFVAVLM	122
	: : : : : : : :	
Db	73 KTDEGHPFKAYLELEITLSQEIQKYTDCLQYVNSTLKELRRLFLVQDLVDSLKFVAVLM	132

Qy	123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP	182
	: :: : : : : :	
Db	133 WLLTYVGALFNGLTLLMAVVSMMFTLPVYYVKHQAQVDQYLGVRTHINTVVAKIQAKIP	192

Qy	183 GLK 185	
	:	
Db	193 GAR 195	

RESULT 4

T26216

hypothetical protein W06A7.3c - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26216
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26216
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2484 <WIL>
A;Cross-references: EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP:W06A7.3c
A;Map position: 5
A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 34.7%; Score 321; DB 2; Length 2484;
Best Local Similarity 32.6%; Pred. No. 1.1e-19;
Matches 60; Conservative 46; Mismatches 78; Indels 0; Gaps 0;

Qy	2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI	61
	: :: : : :: : : : :: ::	
Db	2289 VLDVIYWRDAKKSAIVLSSLALLVLFLAKYPLLTVVTVTYSLLLALGAAAGFRVFKVEAQI	2348
Qy	62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAVL	121
	:: : :: : :: : : : : ::	
Db	2349 KKTDSEHPFSEILAQDLTLPQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKGLV	2408
Qy	122 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI	181
	:: : : : : : : : : : :	
Db	2409 LWSLTYIASWFSGFTLAILGLGVFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKL	2468
Qy	182 PGLK 185	
	:	
Db	2469 PFLR 2472	

RESULT 5

T26215
hypothetical protein W06A7.3a - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26215
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26215
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2607 <WIL>
A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP:W06A7.3a
A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;
2586/2

Query Match 34.7%; Score 321; DB 2; Length 2607;
Best Local Similarity 32.6%; Pred. No. 1.2e-19;
Matches 60; Conservative 46; Mismatches 78; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
|:|::|:||| ||: :| :| :| : ::| | | | | ||::| | | |
Db 2412 VLDVIYWRDAKKSAIVLSSLALLVLFVLAKYPLLTVVTVTYSLLLALGAAAGFRVFKVEAQI 2471

Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAVL 121
:|:| ||| | :: : :| | :: : | :| :| | :| :| | :| :| | :|
Db 2472 KKTDSHPFSEILAQDLTLQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFGLV 2531

Qy 122 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
:| |::| :|:| ||| |:| :|:| :| | | :| | :| | | | | | |
Db 2532 LWSLTYIASWFSGFTLAILGLLGVFSVPKVYESNQEADPHLATISGHLKNVQNIIDEKL 2591

Qy 182 PGLK 185
| |:
Db 2592 PFLR 2595

RESULT 6

T26213

hypothetical protein W06A7.3b - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26213

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26213

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-222 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3b

A;Map position: 5

A;Introns: 27/1; 77/2; 201/2

Query Match 34.6%; Score 320; DB 2; Length 222;
Best Local Similarity 32.1%; Pred. No. 8.5e-21;
Matches 59; Conservative 47; Mismatches 78; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
::|::|:||| ||: :| :| :| : ::| | | | | ||::| | | |
Db 27 ILDVIYWRDAKKSAIVLSSLALLVLFVLAKYPLLTVVTVTYSLLLALGAAAGFRVFKVEAQI 86

Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAVL 121
:|:| ||| | :: : :| | :: : | :| :| | :| :| | :| :| | :|
Db 87 KKTDSHPFSEILAQDLTLQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFGLV 146

Qy 122 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181

```

Db      ::|  ||:: : |||  |||  |: :|||: | :|| :|  || :|  : :||: |  ||:
147  LWSLTYIASWFSGFTLAILGLLGVFSPVKVYESNQEAIIDPHLATISGHLKNVQNIIDEKL 206

Qy      182  PGLK 185
      | |:
Db      207  PFLR 210

```

RESULT 7

E84899

hypothetical protein At2g46170 [imported] - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence revision 02-Feb-2001 #text change 02-Feb-2001

C; Accession: E84899

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A; Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84899

A; Status: preliminary

A;Molecule type: DNA

A;Residues: 1-255 <STO>

A;Cross-references: GB:AE002093; NID:g3702332; PIDN: AAC62889.1; GSPDB:GN00139

C; Genetics:

A;Gene: At2g46170

A;Map position: 2

Query Match 21.0%; Score 194; DB 2; Length 255;
 Best Local Similarity 27.6%; Pred. No. 1.1e-09;
 Matches 54; Conservative 41; Mismatches 77; Indels 24; Gaps 6

Qy	4 DLLYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI	61
	: : ::: : :: : : ::	
Db	70 DVFLWRDKKLSGAVLGVATAIWVLFELVEYHLLSILCHISIILAIG--GLFLWSNAHTLI	12

```

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE LRRFLVVDLVDSLKFAVL 121
       | : | | : : || : | : | || : | | | | | | | |
Ph      127 NKTSPOTP-----EIHVPFFAELVVAASSLPNFILNOAEVILRSIALGRDLKKFELMVAVG 179

```

Qy 122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM----- 174
 :|: : || || |||: : : | ::||:||:||: ::| ||| :||:|:
 Ph 180 LALISLVSAGNWENETLIVIGEYLLWTVPMVYKVKHEDKVD 181 EALKMAMEKQSKVADYR 236

Qy 175 AKIQAKIP--GLKRKA 188
|: :|| || ||

RESULT 9

RESULT
T13013

hypothetical protein F8L21.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 22-Oct-1999
C;Accession: T13013
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.
submitted to the Protein Sequence Database, July 1999
A;Reference number: Z17587
A;Accession: T13013
A;Molecule type: DNA
A;Residues: 1-271 <BEV>
A;Cross-references: EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.10
A;Experimental source: cultivar Columbia; BAC clone F8L21
C;Genetics:
A;Gene: ATSP:F8L21.10
A;Map position: 4
A;Introns: 85/1; 145/2; 192/3; 216/1

Query Match 19.7%; Score 182; DB 2; Length 271;
Best Local Similarity 25.6%; Pred. No. 1.4e-08;
Matches 46; Conservative 43; Mismatches 79; Indels 12; Gaps 3;

Qy	4 DLLYWRDIKKTGVVFGAS--LFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
	: : : : :: : : :: : : ::
Db	87 DIFMWKDKKMSGGVFGGATVAWVLFELMEYHLLTLLCHVMIVALAVLF---LWSNATMFI 143
Qy	62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 121
	: : :: : : :
Db	144 HKSPPKIP-----EVHIPEEPLLQLASGLRIEINRGISSLREIASGRDIKKFLSAIAG 196
Qy	122 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
	: : : :: : :: : :: : : : : :
Db	197 LWVLSILGGCYSFLTAYIALVLLFTVPLFYDKYEDKVDSYGEKAMAELKKQYAVLDAKV 256

RESULT 9

T05595

hypothetical protein F9D16.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05595
R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15419
A;Accession: T05595
A;Molecule type: DNA
A;Residues: 1-275 <BEV>
A;Cross-references: EMBL:AL035394
A;Experimental source: cultivar Columbia; BAC clone F9D16
C;Genetics:
A;Map position: 4
A;Introns: 89/1; 149/2; 196/3; 220/1
A;Note: F9D16.100

Query Match 17.6%; Score 163; DB 2; Length 275;
Best Local Similarity 25.5%; Pred. No. 6.4e-07;

Matches 49; Conservative 43; Mismatches 82; Indels 18; Gaps 5;

Qy 4 DLLYWRDIKKTGVVFG--ASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
 |: |:: | :| | | : ::| | : :::: : :: : ::| :| :| :|

Db 91 DIFMWKNKKMSGGVLGGATAAWVFELMEYHLLTLLCHVMIVVLAVALF---LWSNATMFI 147

Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSKFAVL 121
 || | | | | | : : : : :| | :| | | | |

Db 148 NKSPPKIP-----EVHIPEEPILQLASGLRIEINRGFSSLREIASGRDLKKFLIAIAG 200

Qy 122 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMA---KI 177
 :|| : :| | | | | :||: |::|: |::: :| | :| | | |

Db 201 LWVLSILGGCFNFLTAYIALVLLFTVPLAYDKYEDKVDPLGEKAMIELKKQYAVLDEKV 260

Qy 178 QAKIP--GLKRK 187
 :||| | | |

Db 261 LSKIPLGPLKNK 272

RESULT 10

S67763

probable membrane protein YDL204w - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: hypothetical protein D1062
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
 C;Accession: S67763
 R;Schmidt, E.R.; Bahr, A.; Kraemer, C.; Hankeln, T.; Moeller-Rieker, S.
 submitted to the Protein Sequence Database, July 1996
 A;Reference number: S67756
 A;Accession: S67763
 A;Molecule type: DNA
 A;Residues: 1-393 <SCH>
 A;Cross-references: EMBL:Z74252; NID:g1431337; PID:e253109; PID:g1431338;
 GSPDB:GN00004; MIPS:YDL204w
 A;Experimental source: strain S288C
 C;Genetics:
 A;Gene: MIPS:YDL204w
 A;Cross-references: SGD:S0002363
 A;Map position: 4L
 C;Keywords: transmembrane protein
 F;50-66/Domain: transmembrane #status predicted <TM1>
 F;150-166/Domain: transmembrane #status predicted <TM2>

Query Match 15.4%; Score 142; DB 2; Length 393;
 Best Local Similarity 26.3%; Pred. No. 6.8e-05;
 Matches 45; Conservative 34; Mismatches 56; Indels 36; Gaps 4;

Qy 5 LLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKS 64
 |:|| : |::| | | | | | :|| | :| :|

Db 33 LIYWTNPSKSGASFAATLVSSLILRNVNVISVLLKIGYMLFTS----- 76

Qy 65 DEGHPFRAYLESEVAISEELVQKY---SNSALGHVNSTI-KELRRFLVDDLVDLSKFA 119
 | | ::| : :| :: | :| : | :|| | :| : | |

Db 77 -----FAVELSTKVLFDKGVVSRGMQESPDLGVVLKPHIDRELDRLPALEDRIRKLVFA 131

Qy 120 -----VLMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQID 160
 | :: : |::| : |:||: | |::|:||:| | :|

Db 132 HRTRNNFTIGVSLYFLHGLFAIFSMNTVLIMTTIFLYTVPLIYDRKQARID 182

RESULT 11

B85016

hypothetical protein AT4g01230 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C;Accession: B85016

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor, Washington University in St Louis and PE Biosystems Arabidopsis Sequencing Consortium.

Nature 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: B85016

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-242 <STO>

A;Cross-references: GB:NC_001268; NID:g7267620; PIDN: CAB80932.1; GSPDB:GN00140

C;Genetics:

A;Gene: AT4g01230

A;Map position: 4

Query Match 14.6%; Score 135.5; DB 2; Length 242;
Best Local Similarity 23.8%; Pred. No. 0.00014;
Matches 46; Conservative 49; Mismatches 63; Indels 35; Gaps 7;

Qy 4 DLLYWRDIKKTGVVFGASLFLLLSLTVFSIV-----SVTAYIALALLSVTISFRIYKG 56
|:| ||| | | | | || ::|| :: :|: ::| : :|| ::
Db 70 DVLLWRDKKV-----LGLLSAVTVIWLLFGFGGRRLLTSLCRGSILFLLSF-LWS- 120

Qy 57 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSL 116
|:| ||| ::| |: : : :: :| || :| |: :| :
Db 121 --NALNKSPEN-----MMDIYIPEKPLLQAASAMTFELNCAFATLRSIALERDIKNFV 171

Qy 117 KFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM-- 174
: :|: :| |: |:|| : : : :|:||: :| || :| :| :
Db 172 MAVIGLWLVSIGNWFSFLSLLYICFVLIHTVPMLYEKYEDEID---PIAEKAVIEMKKH 228

Qy 175 -----AKIQAKIP 182
|| :|||

Db 229 YQVFEAKFLSKIP 241

RESULT 12

A84527

hypothetical protein At2g15280 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84527

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver,

G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84527
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <STO>
A;Cross-references: GB:AE002093; NID:g4662633; PIDN:AAD26905.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g15280
A;Map position: 2

```

Query Match           14.5%;  Score 134;  DB 2;  Length 183;
Best Local Similarity 24.6%;  Pred. No. 0.00014;
Matches 44;  Conservative 38;  Mismatches 79;  Indels 18;  Gaps 4;
Y          8 WRDIKKTGVVFGAS----LFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
|:: : :: |:: || : | | : |||| | | | |
D          2 WKNRRGGFLLLGSSTLLWFLFEKCGYSFFPV----VNTQLLSVVILFLWAKSAI---- 52
Y          63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAVLM 122
: | || | :|| | :: :| : | :: : :| :|| :| :|| :
D          53 LFNRPMPQLPNLE----ITEEFVFMVADAIRWINTVLAVAREIYVGRNAKQLFRVSVVL 108
Y          123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
| :|| | ||:| | :: || :||:| || | | :: :| | :|
D          109 WTVSFVGNFLNFLTILYLGVVLSLLIPFLYERYQDLIDEKLSLTHRVIQTQYRKIDERL 167

```

RESULT 13

S59439

probable membrane protein YDR233c - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein YD9934.17c

C;Species: *Saccharomyces cerevisiae*

C;Date: 30-Nov-1995 #sequence revision 16-Feb-1996 #text change 19-Apr-2002

C;Accession: S59439

R;Murphy, L.; Harris, D.

submitted to the EMBL Data Library, March 1995

A; Reference number: S59423

A:Accession: S59439

A: Molecule type: DNA

A:Residues: 1-295 <MIIB>

A:Cross-references: EMBL:Z48612; NID:G728671; PID:G728688; CSBDB:CN00004;

MTBS:YDR233c

A:Experimental source: strain AB972

A. Erfahrungen S: Sonatissen

2. Genetics:

A;Gene: M1PS:YDR233c

A; Cross-references:

A;Map position: 4R

C;Keywords: transmembrane protein

F;40-56/Domain: transmembrane #status predicted <TM1>

Open Access Methods 2019, 14:88 DOI: 10.1186/s13021-019-0057-1

Best Local Similarity 21.6%; Pred. No. 0.0004;
Matches 45; Conservative 43; Mismatches 69; Indels 51; Gaps 5;

Qy 4 DLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQK 63
||| ||: :|| || || || | :::: :| :| | | | : :
Db 22 DLLLWRNPVQTGKYFGGSLLALLLKKVNLTFFLKVAYTILFTT-----GSIEFV-- 72
Qy 64 SDEGHPFRAYLESEVAISEELVQKY-----SNSALGHVNSTIKEL-----RRLFL 108
|:: : : |: || : |:: :|: |: |: |: |:
Db 73 -----SKLFLGQGLITKYGPKECPNIAGFIKPHIDEALKQLPVFQAHIRKTVF 120
Qy 109 VDDLVDLSLKFAVLMWVFTYVGALFNGLTLLALISLFSIPVIYERHQVQID----- 160
: | || ::: : |: |:: :| | |::| ||| | : : |||
Db 121 AQVPKHTFKTAVALFLLHKFFSWFSIWTIVFVADIFTFLPVIYHSYKHEIDATVAQGVE 180
Qy 161 -----HYLGLANKSVKDAMAKIQAKI 181
: | : | : |::|:
Db 181 ISKQKTQEFQMACEKTPYLDKVESKL 208

RESULT 14

T01153

probable seed maturation protein [imported] - *Arabidopsis thaliana*
N;Alternate names: hypothetical protein F27L4.17
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C;Accession: T01153; T02426; C84627
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.;
Venter, J.C.
submitted to the EMBL Data Library, June 1998
A;Description: *Arabidopsis thaliana* chromosome II BAC F26B6 genomic sequence.
A;Reference number: Z14198
A;Accession: T01153
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-206 <ROU>
A;Cross-references: EMBL:AC003040; NID:g3242700; PID:g3242725
A;Experimental source: cultivar Columbia
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.;
Venter, J.C.
submitted to the EMBL Data Library, May 1998
A;Description: *Arabidopsis thaliana* chromosome II BAC F27L4 genomic sequence.
A;Reference number: Z14658
A;Accession: T02426
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-206 <RO2>
A;Cross-references: EMBL:AC004482; NID:g3152602; PIDN: AAC17096.1; PID:g3152617
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;
Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell,
C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin,
L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams,
M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver,
G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser,
C.M.; Venter, J.C.

RESULT 15
T47948
hypothetical protein F2A19.160 - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47948
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z24480
A;Accession: T47948
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 <DEH>
A;Cross-references: EMBL:AL132962
A;Experimental source: cultivar Columbia; BAC clone F2A19
C;Genetics:
A;Map position: 3
A;Introns: 68/1; 128/2; 164/1; 210/1
A;Note: F2A19.160

Query Match 11.8%; Score 109.5; DB 2; Length 264;
Best Local Similarity 24.9%; Pred. No. 0.03;
Matches 54; Conservative 38; Mismatches 68; Indels 57; Gaps 14;

Qy	4 DLLYWRDIKKTGVVFG--ASLFLLSLTVFSIVSVTAYI-----ALALLSVTISFRIYK 55
: : :::: : : : : : :	
Db	70 DVFLWRDKKLSASVLGVATAIWVLFELVEYHFLSLVCHILIFALAALFLLSNAHAF-MNK 128
Qy	56 GVIQ-----AIQKSDEG-----HPFRAYLESEVAISEELVQK-YSN-SALGHVNSTIKE 102
::::: : :	
Db	129 GTFPYDCFCTEKRAEPGLCYFKEHCLRKGLEE---ISHELIQSTYETFSIMGFVTRT--- 182
Qy	103 LRRFLVDDLVDLSLKFAVL--MWVFTYVGALFNG--LTLLILALISLFSIPVIYERHQVQ 158
: : : : : :: : : :	
Db	183 -----SIYIGISGGFWAVDNLGC---GKLVQLLDSCFVVLHTVPMLYEKHEDK 227
Qy	159 IDHYLGLANKSVKDAM-----AKIQAKIPGLKRKA 188
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Db	228 VD---PVAEKTALKELKKHYMVFDEKVLSKLPVASLKA 261

Search completed: September 29, 2004, 18:15:52

Job time : 6.62587 secs

1	925	100.0	1163	9	US-09-893-348-18	Sequence 18, Appl
2	922	99.7	379	14	US-10-205-194-164	Sequence 164, App
3	921	99.6	199	9	US-09-893-348-21	Sequence 21, Appl
4	921	99.6	360	9	US-09-893-348-20	Sequence 20, Appl
5	908	98.2	1192	9	US-09-789-386-2	Sequence 2, Appli
6	908	98.2	1192	9	US-09-758-140-6	Sequence 6, Appli
7	908	98.2	1192	9	US-09-893-348-23	Sequence 23, Appl
8	908	98.2	1192	9	US-09-972-599A-6	Sequence 6, Appli
9	908	98.2	1192	12	US-10-267-502-429	Sequence 429, App
10	908	98.2	1192	14	US-10-060-036-71	Sequence 71, Appl
11	908	98.2	1192	16	US-10-327-213-9	Sequence 9, Appli
12	908	98.2	1192	16	US-10-466-258-9	Sequence 9, Appli
13	906.5	98.0	1163	12	US-10-267-502-431	Sequence 431, App
14	904	97.7	199	9	US-09-893-348-25	Sequence 25, Appl
15	904	97.7	199	12	US-10-660-946-1	Sequence 1, Appli
16	904	97.7	373	9	US-09-789-386-6	Sequence 6, Appli
17	904	97.7	373	9	US-09-765-205-6	Sequence 6, Appli
18	904	97.7	373	9	US-09-893-348-24	Sequence 24, Appl
19	904	97.7	373	12	US-10-408-967-8	Sequence 8, Appli
20	904	97.7	373	14	US-10-060-036-72	Sequence 72, Appl
21	904	97.7	373	16	US-10-466-258-4	Sequence 4, Appli
22	901	97.4	1192	12	US-10-408-967-7	Sequence 7, Appli
23	897	97.0	199	12	US-10-408-967-9	Sequence 9, Appli
24	895	96.8	199	12	US-09-978-360A-467	Sequence 467, App
25	864	93.4	199	16	US-10-466-258-11	Sequence 11, Appl
26	679	73.4	208	12	US-10-660-946-7	Sequence 7, Appli
27	679	73.4	356	12	US-10-660-946-6	Sequence 6, Appli
28	679	73.4	776	12	US-10-660-946-5	Sequence 5, Appli
29	679	73.4	776	12	US-10-267-502-430	Sequence 430, App
30	678	73.3	777	14	US-10-205-219-93	Sequence 93, Appl
31	678	73.3	780	12	US-10-267-502-432	Sequence 432, App
32	665	71.9	267	12	US-10-660-946-8	Sequence 8, Appli
33	665	71.9	267	14	US-10-205-194-127	Sequence 127, App
34	622.5	67.3	236	9	US-09-729-674-20	Sequence 20, Appl
35	622.5	67.3	236	9	US-09-765-205-26	Sequence 26, Appl
36	622.5	67.3	236	12	US-10-408-967-2	Sequence 2, Appli
37	622.5	67.3	266	12	US-10-276-774-2330	Sequence 2330, Ap
38	622.5	67.3	269	14	US-10-106-698-6222	Sequence 6222, Ap
39	617.5	66.8	593	15	US-10-108-260A-2892	Sequence 2892, Ap
40	539.5	58.3	168	10	US-09-809-391-563	Sequence 563, App
41	539.5	58.3	168	10	US-09-882-171-563	Sequence 563, App
42	539.5	58.3	168	12	US-10-164-861-563	Sequence 563, App
43	520	56.2	222	12	US-10-267-502-428	Sequence 428, App
44	516	55.8	241	12	US-10-660-946-3	Sequence 3, Appli
45	507.5	54.9	234	12	US-10-424-599-200840	Sequence 200840,

ALIGNMENTS

RESULT 1
 US-09-893-348-18
 ; Sequence 18, Application US/09893348
 ; Patent No. US20020072493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EISENBACK-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18

Query Match 100.0%; Score 925; DB 9; Length 1163;
Best Local Similarity 100.0%; Pred. No. 1e-84;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA	60
Db	975	SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA	1034
Qy	61	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV	120
Db	1035	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV	1094
Qy	121	LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK	180
Db	1095	LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK	1154
Qy	181	IPGLKRKAD 189	
Db	1155	IPGLKRKAD 1163	

RESULT 2

US-10-205-194-164

; Sequence 164, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Foocen-m2 reticulon
US-10-205-194-164

Query Match 99.7%; Score 922; DB 14; Length 379;
Best Local Similarity 99.5%; Pred. No. 4.6e-85;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQ 60
:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 191 AVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQ 250

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE LRRFLVDDLVDSDLKFAV 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 251 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE LRRFLVDDLVDSDLKFAV 310

Qy 121 LMWVFTYVGALFNGLTL LALISLFSIPVIYERHQVQIDH YLGLANKSVKDAMAKI QAK 180
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 311 LMWVFTYVGALFNGLTL LALISLFSIPVIYERHQVQIDH YLGLANKSVKDAMAKI QAK 370

Qy 181 IPGLKRKAD 189
||||||||||
Db 371 IPGLKRKAD 379

RESULT 3

US-09-893-348-21

; Sequence 21, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISEN BACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-21

Query Match 99.6%; Score 921; DB 9; Length 199;
Best Local Similarity 100.0%; Pred. No. 2.5e-85;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI	61
Db	12	VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI	71
Qy	62	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSKFAVL	121
Db	72	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSKFAVL	131
Qy	122	MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI	181
Db	132	MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI	191
Qy	182	PGLKRKAD 189	
Db	192	PGLKRKAD 199	

RESULT 4

US-09-893-348-20

; Sequence 20, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACK-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20

Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV 120
 |||||||
 Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSDLKFAV 1123
 Qy 121 LMWVFTYVGALFNGLTLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
 |||||||
 Db 1124 LMWVFTYVGALFNGLTLALISLFSVPVIYERHQQAQIDHYLGLANKNVKDAMAKIQAK 1183
 Qy 181 IPGLKRKAD 189
 |||||||:
 Db 1184 IPGLKRKAE 1192

RESULT 6

US-09-758-140-6

; Sequence 6, Application US/09758140
 ; Patent No. US20020012965A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Strittmatter, Stephen M.
 ; TITLE OF INVENTION: No. US20020012965A1 o Receptor-Mediated Blockade of
 Axonal Growth
 ; FILE REFERENCE: 44574-5073-US
 ; CURRENT APPLICATION NUMBER: US/09/758,140
 ; CURRENT FILING DATE: 2001-01-12
 ; PRIOR APPLICATION NUMBER: US 60/175,707
 ; PRIOR FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: US 60/207,366
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/236,378
 ; PRIOR FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 1192
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-758-140-6

Query Match 98.2%; Score 908; DB 9; Length 1192;
 Best Local Similarity 97.4%; Pred. No. 5.5e-83;
 Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
 |||||||
 Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV 120
 |||||||
 Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSDLKFAV 1123
 Qy 121 LMWVFTYVGALFNGLTLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
 |||||||
 Db 1124 LMWVFTYVGALFNGLTLALISLFSVPVIYERHQQAQIDHYLGLANKNVKDAMAKIQAK 1183
 Qy 181 IPGLKRKAD 189

|||||||:
Db 1184 IPGLKRKAE 1192

RESULT 7
US-09-893-348-23
; Sequence 23, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACK-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-23

Query Match 98.2%; Score 908; DB 9; Length 1192;
Best Local Similarity 97.4%; Pred. No. 5.5e-83;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063
Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFVDDLVDSLKF 120
Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFVDDLVDSLKF 1123
Qy 121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
Db 1124 LMWVFTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183
Qy 181 IPGLKRKAD 189
Db 1184 IPGLKRKAE 1192

RESULT 8

US-09-972-599A-6
; Sequence 6, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

RESULT 9
US-10-267-502-429
; Sequence 429, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416

; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 429
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-429

Query Match 98.2%; Score 908; DB 12; Length 1192;
Best Local Similarity 97.4%; Pred. No. 5.5e-83;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 61 IOKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFVDDLVDSDLKFAV 120
|||||
Ph 1064 IOKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFVDDLVDSDLKFAV 120

Qy 181 IPGLKRKAD 189
|||:|||:
Pb 1184 TPGLKRKAE 1192

RESULT 10

US-10-060-036-71

; Sequence 71, Application US/10060036

; Publication No. US20

; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Liang, Yunjin

; APPLICANT: Jiang, Jiaqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

FILE REFERENCE: 210121-566

CURRENT APPLICATION NUMBER: US/10/060,036

CURRENT FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 71

; LENGTH: 1192

; TYPE: PRT

; ORGANISM:

US-10-060-036-71

Best Local Similarity 97.4%; Pred. No. 5.5e-83;

Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSDLKFAV 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDSDLKFAV 1123

Qy 121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
 ||||||||||||||||||||:|||||||| ||||||||||||:|||||||||||

Db 1124 LMWVFTYVGALFNGLTLILALISLFSVPVIYERHQQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy 181 IPGLKRKAD 189
 |||||||:

Db 1184 IPGLKRKAE 1192

RESULT 11

US-10-327-213-9

; Sequence 9, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
; APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-327-213-9

Query Match 98.2%; Score 908; DB 16; Length 1192;
 Best Local Similarity 97.4%; Pred. No. 5.5e-83;
 Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
 |||||||||||||||||||||||||||||||||||||||||||||||

Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSDLKFAV 120
 |||||||||||||||||||||||||||||||||||||||||||

Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDSDLKFAV 1123

Qy 121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
 ||||||||||||||||||||:|||||||| ||||||||||||:|||||||||||

Db 1124 LMWVFTYVGALFNGLTLILALISLFSVPVIYERHQQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy 181 IPGLKRKAD 189

|||||||:
Db 1184 IPGLKRKAE 1192

RESULT 12
US-10-466-258-9
; Sequence 9, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-258-9

Query Match 98.2%; Score 908; DB 16; Length 1192;
Best Local Similarity 97.4%; Pred. No. 5.5e-83;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQ 60
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQ 1063
Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKF 120
|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDSLKF 1123
Qy 121 LMWVFTYVGALFNGLTLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ 180
|||||||||||||||||||||:|||||:|||||:|||||:|||||:|||||
Db 1124 LMWVFTYVGALFNGLTLLALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 1183
Qy 181 IPGLKRKAD 189
|||||||:
Db 1184 IPGLKRKAE 1192

RESULT 13
US-10-267-502-431
; Sequence 431, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 431

; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-267-502-431

Query Match 98.0%; Score 906.5; DB 12; Length 1163;
Best Local Similarity 98.4%; Pred. No. 7.6e-83;
Matches 187; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SVVDLLYWRDIKKTGVV-FGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 59
Db 974 SVVDLLYWRDIKKTGVVYFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 1033

Qy 60 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFA 119
Db 1034 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFA 1093

Qy 120 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA 179
Db 1094 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA 1153

Qy 180 KIPGLKRKAD 189
Db 1154 KIPGLKRKAE 1163

RESULT 14

US-09-893-348-25

; Sequence 25, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACK-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-25

Query Match 97.7%; Score 904; DB 9; Length 199;
 Best Local Similarity 97.3%; Pred. No. 1.3e-83;
 Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy	2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI	61
Db	12 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI	71
Qy	62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL	121
Db	72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL	131
Qy	122 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI	181
	: :	
Db	132 MWVFTYVGALFNGLTLILALISLFSVPVIYERHQVQIDHYLGLANKNVKDAMAKIQAKI	191
Qy	182 PGLKRKAD 189	
	:	
Db	192 PGLKRKAE 199	

RESULT 15

US-10-660-946-1

; Sequence 1, Application US/10660946
 ; Publication No. US20040063131A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; Au-Young, Janice
 ; Goli, Surya K.
 ; Hillman, Jennifer L.
 ; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/660,946
 ; FILING DATE: 12-Sep-2003
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/228,213A
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 08/700,607
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0114 US
 ; TELECOMMUNICATION INFORMATION:

;
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-660-946-1

Query Match 97.7%; Score 904; DB 12; Length 199;
Best Local Similarity 97.3%; Pred. No. 1.3e-83;
Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 12 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 121
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 131

Qy 122 MWVFTYVGALFNGLTLLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
||| ||| ||| ||| ||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| : ||| ||| |||
Db 132 MWVFTYVGALFNGLTLLLALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy 182 PGLKRKAD 189
||| ||| :
Db 192 PGLKRKAE 199

Search completed: September 29, 2004, 18:48:12
Job time : 21.2878 secs

1	917	99.1	578	11	Q80W95	Q80w95 mus musculu
2	917	99.1	639	11	Q8K290	Q8k290 mus musculu
3	917	99.1	1046	11	Q8BGK7	Q8bgk7 mus musculu
4	917	99.1	1162	11	Q8BGM9	Q8bgm9 mus musculu
5	914	98.8	375	11	Q8BHF5	Q8bhf5 mus musculu
6	913	98.7	356	11	Q8BH78	Q8bh78 mus musculu
7	908	98.2	986	4	Q8IUA4	Q8iua4 homo sapien
8	906.5	98.0	1163	11	Q8K3G8	Q8k3g8 mus musculu
9	905	97.8	392	4	Q96B16	Q96b16 homo sapien
10	902.5	97.6	357	11	Q8K3G7	Q8k3g7 mus musculu
11	878	94.9	184	6	Q7YRW9	Q7yrw9 bos taurus
12	872	94.3	199	13	Q7T224	Q7t224 gallus gall
13	844	91.2	179	6	Q9GM33	Q9gm33 macaca fasc
14	733	79.2	214	13	Q7T222	Q7t222 carassius a
15	679	73.4	199	4	Q9BQ59	Q9bq59 homo sapien
16	678	73.3	780	11	Q8K4S4	Q8k4s4 mus musculu
17	678	73.3	780	11	Q8K0T0	Q8k0t0 mus musculu
18	669	72.3	760	13	Q90638	Q90638 gallus gall
19	665	71.9	208	13	Q90637	Q90637 gallus gall
20	665	71.9	267	11	Q63765	Q63765 rattus sp.
21	622.5	67.3	236	11	Q8VBU0	Q8vbu0 rattus norv
22	622.5	67.3	237	11	Q8C6D5	Q8c6d5 mus musculu
23	621.5	67.2	643	11	Q8CCU2	Q8ccu2 mus musculu
24	581	62.8	221	13	Q7ZUD6	Q7zud6 brachydanio
25	521	56.3	224	5	Q9VMW1	Q9vmw1 drosophila
26	520	56.2	222	5	Q9VMW4	Q9vmw4 drosophila
27	520	56.2	234	5	Q9VMW3	Q9vmw3 drosophila
28	520	56.2	595	5	Q9VMV9	Q9vmv9 drosophila
29	518	56.0	202	5	Q9VMW2	Q9vmw2 drosophila
30	344	37.2	107	13	Q7T223	Q7t223 carassius a
31	321	34.7	2484	5	Q9U347	Q9u347 caenorhabdi
32	321	34.7	2607	5	Q23187	Q23187 caenorhabdi
33	320	34.6	222	5	Q23188	Q23188 caenorhabdi
34	198.5	21.5	154	5	Q9VIB7	Q9vib7 drosophila
35	198.5	21.5	158	5	Q24199	Q24199 drosophila
36	194	21.0	255	10	Q82352	Q82352 arabidopsis
37	189	20.4	255	10	Q9SH59	Q9sh59 arabidopsis
38	182	19.7	271	10	Q9SUT9	Q9sut9 arabidopsis
39	170	18.4	257	10	Q9FFS0	Q9ffs0 arabidopsis
40	163	17.6	275	10	Q9SUR3	Q9sur3 arabidopsis
41	160	17.3	200	10	Q9LT71	Q9lt71 arabidopsis
42	158	17.1	200	10	Q8LAT8	Q8lat8 arabidopsis
43	158	17.1	279	10	Q9AWY7	Q9awy7 oryza sativ
44	154.5	16.7	192	10	Q7XR59	Q7xr59 oryza sativ
45	154	16.6	253	10	Q8S2K0	Q8s2k0 oryza sativ

ALIGNMENTS

RESULT 1

Q80W95

ID Q80W95 PRELIMINARY; PRT; 578 AA.
 AC Q80W95;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Nogo-A (Fragment).
 GN NOGO-A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tozaki H., Hirata T.;
 RT "The partial sequence of mouse nogo-A cDNA clone#4109.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB073672; BAC75974.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

 Query Match 99.1%; Score 917; DB 11; Length 578;
 Best Local Similarity 98.9%; Pred. No. 2.5e-72;
 Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
 |||||||
 Db 390 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 449

 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAV 120
 |||||||
 Db 450 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAV 509

 Qy 121 LMWVFTYVGALFNGLTLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
 |||||||
 Db 510 LMWVFTYVGALFNGLTLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 569

 Qy 181 IPGLKRKAD 189
 |||||:
 Db 570 IPGLKRKAE 578

RESULT 2
 Q8K290
 ID Q8K290 PRELIMINARY; PRT; 639 AA.
 AC Q8K290;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC032192; AAH32192.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

 Query Match 99.1%; Score 917; DB 11; Length 639;
 Best Local Similarity 98.9%; Pred. No. 2.8e-72;
 Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQ 60
 |||||||
 Db 451 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQ 510

 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV 120
 |||||||
 Db 511 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV 570

 Qy 121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
 |||||||
 Db 571 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 630

 Qy 181 IPGLKRKAD 189
 |||||:
 Db 631 IPGLKRKAE 639

RESULT 3
 Q8BGK7
 ID Q8BGK7 PRELIMINARY; PRT; 1046 AA.
 AC Q8BGK7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RTN4.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129SvcJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY102280; AAM73502.1; -.
DR EMBL; AY102286; AAM73507.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 99.1%; Score 917; DB 11; Length 1046;
Best Local Similarity 98.9%; Pred. No. 4.9e-72;
Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
Db 858 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 917

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120
Db 918 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 977

Qy 121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
Db 978 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1037

Qy 181 IPGLKRKAD 189
Db 1038 IPGLKRKAE 1046

RESULT 4

Q8BGM9

ID Q8BGM9 PRELIMINARY; PRT; 1162 AA.
AC Q8BGM9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RTN4.
GN RTN4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvcJ7;
RA Oertle T., van der Putten H., Schwab M.E.;

GN RTN4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvcJ7;
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
Structures of Human and Mouse Nogo/Rtn-4.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvcJ7;
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129SvcJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY102282; AAM73504.1; -.
DR EMBL; AY102286; AAM73509.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;

Query Match 98.8%; Score 914; DB 11; Length 375;
Best Local Similarity 98.4%; Pred. No. 2.8e-72;
Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 187 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 246

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAV 120
|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 247 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAV 306

Qy 121 LMWVFTYVGALFNGLTLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
|||||||||||||||||||||||||||||||||
Db 307 LMWVFTYVGALFNGLTLLALISLFSIPVIYERHQQAQIDHYLGLANKSVKDAMAKIQAK 366

Qy 181 IPGLKRKAD 189
|||||||:
Db 367 IPGLKRKAE 375

RESULT 6

Q8BH78

ID Q8BH78 PRELIMINARY; PRT; 356 AA.
AC Q8BH78;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RTN4.
GN RTN4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvcJ7;
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7, and 129SvcJ7;
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]

RP SEQUENCE FROM N.A.
RC STRAIN=129SvcJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY102281; AAM73503.1; -.
DR EMBL; AY102286; AAM73508.1; -.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 98.7%; Score 913; DB 11; Length 356;
Best Local Similarity 98.9%; Pred. No. 3.3e-72;
Matches 186; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 169 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 228
QY 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 229 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 288

Qy 122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
||||||||||||||||||||||||||||||||||||||||||||||||
Db 289 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 348
Qy 182 PGLKRKAD 189
||||||:
Db 349 PGLKRKAE 356

RESULT 7

Q8IUA4

ID Q8IUA4 PRELIMINARY; PRT; 986 AA.
AC Q8IUA4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RNT4 (RTN4).
GN RTN4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
Structures of Human and Mouse Nogo/Rtn-4.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22376540; PubMed=12488097;
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
Structures of Human and Mouse Nogo/Rtn-4.";
RL J. Mol. Biol. 325:299-323(2003).
DR EMBL; AY102285; AAM64244.1; -.
DR EMBL; AY123245; AAM64249.1; -.
DR EMBL; AY123246; AAM64250.1; -.
DR EMBL; AY123247; AAM64251.1; -.
DR EMBL; AY123248; AAM64252.1; -.
DR EMBL; AY123249; AAM64253.1; -.
DR EMBL; AY123250; AAM64254.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;

Query Match 98.2%; Score 908; DB 4; Length 986;
 Best Local Similarity 97.4%; Pred. No. 2.8e-71;
 Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
 |||||||
 Db 798 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 857

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV 120
 |||||||
 Db 858 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSDLKFAV 917

Qy 121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
 |||||||:||||||:||||||:||||||:||||||:||||||:||||||:||||||:||||||:||||||:
 Db 918 LMWVFTYVGALFNGLTLILALISLFSVPVIYERHQVQIDHYLGLANKNVKDAMAKIQAK 977

Qy 181 IPGLKRKAD 189
 |||||||:
 Db 978 IPGLKRKAE 986

RESULT 8

Q8K3G8

ID Q8K3G8 PRELIMINARY; PRT; 1163 AA.
 AC Q8K3G8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nogo-A.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Jin W., Long M., Li R., Ju G.;
 RT "Cloning and expression of the mouse Nogo-A protein.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY114152; AAM77068.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 1163 AA; 126691 MW; 6B5F362799417EA4 CRC64;

Query Match 98.0%; Score 906.5; DB 11; Length 1163;
 Best Local Similarity 98.4%; Pred. No. 4.6e-71;
 Matches 187; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 59
 |||||||
 Db 974 SVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 1033

QY 60 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFA 119
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1034 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFA 1093
QY 120 VLMWVFTYVGALFNGLTLLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA 179
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1094 VLMWVFTYVGALFNGLTLLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA 1153
QY 180 KIPGLKRKAD 189
||| ||| |||:
Db 1154 KIPGLKRKAE 1163

RESULT 9

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.
AC Q96B16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (RTN4).
GN RTN4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Oertle T., Schwab M.E.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22376540; PubMed=12488097;
RA Oertle T., van der Putten H., Schwab M.E.;
RT "Genomic Structure and Functional Characterization of the Promoter
RT Structures of Human and Mouse Nogo/Rtn-4.";
RL J. Mol. Biol. 325:299-323(2003).
DR EMBL; BC016165; AAH16165.1; -.
DR EMBL; AY102285; AAM64242.1; -.
DR EMBL; AY102278; AAM64247.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.

DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

 Query Match 97.8%; Score 905; DB 4; Length 392;
 Best Local Similarity 96.8%; Pred. No. 1.8e-71;
 Matches 183; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

 Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
 :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 204 AVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 263

 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 264 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSDLKFAV 323

 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
 ||||||||||||||||||||||:||||||| |||||||||||:|||||||||||
 Db 324 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQVQIDHYLGLANKNVKDAMAKIQAK 383

 Qy 181 IPGLKRKAD 189
 |||||||:
 Db 384 IPGLKRKAE 392

RESULT 10
 Q8K3G7
 ID Q8K3G7 PRELIMINARY; PRT; 357 AA.
 AC Q8K3G7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nogo-B.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Jin W., Li R., Long M., Shen J., Ju G.;
 RT "Cloning and expression of the mouse Nogo-B protein.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY114153; AAM77069.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

Query Match 97.6%; Score 902.5; DB 11; Length 357;
 Best Local Similarity 98.4%; Pred. No. 2.8e-71;

Matches 186; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 2 VVDLLYWRDIKKTGVV-FGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
 ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||

Db 169 VVDLLYWRDIKKTGVVYFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 228

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 229 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 288

Qy 121 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||

Db 289 LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 348

Qy 181 IPGLKRKAD 189
 |||||||:
Db 349 IPGLKRKAE 357

RESULT 11

Q7YRW9

ID Q7YRW9 PRELIMINARY; PRT; 184 AA.
AC Q7YRW9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RTN4w (Fragment).
GN RTN4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22715887; PubMed=12832288;
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
RT RTN/Nogo gene family.";
RL FASEB J. 17:1238-1247(2003).
DR EMBL; AY164744; AAP47319.1; -.
FT NON_TER 1 1
SQ SEQUENCE 184 AA; 20671 MW; DE990E03BBAF84A1 CRC64;

Query Match 94.9%; Score 878; DB 6; Length 184;
Best Local Similarity 96.2%; Pred. No. 1.9e-69;
Matches 177; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 6 LYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSD 65
 ||||||||||||||| |||||||||||||||||||||||||||||||||||||

Db 1 LYWRDIKKTGVVFGXXLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSD 60

Qy 66 EGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWF 125
 |||||||||||||||||||||||||||||||||||||||||||||||

Db 61 EGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWF 120

Qy 126 TYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLK 185

Db 121 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 121 TYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 180
 Qy 186 RKAD 189
 |||:
 Db 181 RKAЕ 184

RESULT 12

Q7T224

ID Q7T224 PRELIMINARY; PRT; 199 AA.
 AC Q7T224;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RTN4-C.
 GN RTN4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22715887; PubMed=12832288;
 RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
 RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
 RT RTN/Nogo gene family.";
 RL FASEB J. 17:1238-1247(2003).
 DR EMBL; AY164737; AAP47312.1; -.
 SQ SEQUENCE 199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;

Query Match 94.3%; Score 872; DB 13; Length 199;
 Best Local Similarity 91.5%; Pred. No. 6.9e-69;
 Matches 172; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
 |||||||:|||||:
 Db 12 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71
 |||||||:
 Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAVL 121
 |||||||:
 Db 72 QKSDEGHPFRAYLESNAVSEDLIQKYSSVVLGHINGTVKELRRLFLVDDLVDSDLKFAVL 131
 |||||||:
 Qy 122 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
 |||||||:
 Db 132 MWVFTYVGALFNGLTLILALISLFSVPVIYERHQAQIDHYLGLVNKNVKDAMAKIQAKI 191
 |||||||:
 Qy 182 PGLKRKAD 189
 |||||||:
 Db 192 PGLKRKTE 199

RESULT 13

Q9GM33

ID Q9GM33 PRELIMINARY; PRT; 179 AA.
 AC Q9GM33;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB049853; BAB16739.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Hypothetical protein.
SQ SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;

Query Match 91.2%; Score 844; DB 6; Length 179;
Best Local Similarity 95.5%; Pred. No. 1.8e-66;
Matches 171; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 11 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPF 70
:|||||||||||||||||||||||||||||:|||||||||||||
Db 1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVIQAIQKSDEGHPF 60

Qy 71 RAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAVLMWVFTYVGA 130
|||||||||||||||||||||:|||||||||:|||||||||
Db 61 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSDLRFAVLMWVFTYVGA 120

Qy 131 LFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 189
|||||||||||||:|||||||:|||||||||:|||||||||
Db 121 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 179

RESULT 14

Q7T222

ID Q7T222 PRELIMINARY; PRT; 214 AA.
AC Q7T222;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RTN4-M.
GN RTN4.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=22715887; PubMed=12832288;
 RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
 RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the
 RTN/Nogo gene family.";
 RL FASEB J. 17:1238-1247(2003).
 DR EMBL; AY164754; AAP47329.1; -.
 SQ SEQUENCE 214 AA; 24063 MW; E9B603B043159DD9 CRC64;

 Query Match 79.2%; Score 733; DB 13; Length 214;
 Best Local Similarity 73.4%; Pred. No. 1.3e-56;
 Matches 138; Conservative 25; Mismatches 25; Indels 0; Gaps 0;

 QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
 |||||||:|||||:|||||:|||||:|||:|||:||:|||||||||:|||||:
 Db 27 VVDLLYWRDLQRTGVVFGASLLLLSLSVCSIISVISYVALALLSVTISFRIYKGILQAV 86

 QY 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
 ||||:||||:||:||:|||:|||||:|||:|||:|||||:|||||:
 Db 87 QKSEDGHPFKMYLDKDIGISSELVQKYSDTALAHINCVIKELRRLFLVEDLVDSLKFAVF 146

 Qy 122 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
 ||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 147 MWILTYVGALFNGLTLIMGLIGTFSWPVIYEKHQAQIDHYYGLVNKQIKDVMGKIQAKI 206

 Qy 182 PGLKRKAD 189
 ||| :
 Db 207 PGAKPKTE 214

RESULT 15

Q9BQ59
 ID Q9BQ59 PRELIMINARY; PRT; 199 AA.
 AC Q9BQ59;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to reticulon 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC003003; AAH03003.1; -.
 DR EMBL; BC000314; AAH00314.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR GO; GO:0000786; C:nucleosome; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; IEA.
 DR GO; GO:0006334; P:nucleosome assembly; IEA.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS00047; HISTONE_H4; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22642 MW; 7CFA44CC568DF6D8 CRC64;

Query Match 73.4%; Score 679; DB 4; Length 199;
Best Local Similarity 67.9%; Pred. No. 6.6e-52;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

Qy 3 VDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
:||||||||:||:||:|:| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :||:|:
Db 13 IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVAYLALAALSATISFRIYKSVLQAVQ 72

Qy 63 KSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRRLFLVDDLVDSLKFVLM 122
|:|||||||:||||| |: :||| :|||:: :||||:||||||||| ||||||||||| |||||||||||
Db 73 KTDEGHPPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELELRRRLFLVQDLVDSLKFVLM 132

Qy 123 WVFTYVGALFNGLTLLILALISLFSIPVYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
|:|||||||||:||:||:||:||:||:|| :|| ||| ||| ||| : :||| ||| ||| |||
Db 133 WLLTYVGALFNGLTLLIMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 192

Qy 183 GLKRKAD 189
| || |:
Db 193 GAKRHAE 199

Search completed: September 29, 2004, 18:19:40
Job time : 15.8689 secs

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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:04:48 ; Search time 2.70944 Seconds
(without alignments)
3632.211 Million cell updates/sec

Title: US-09-830-972-2_COPY_975_1163
Perfect score: 925
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	925	100.0	1163	1	RTN4_RAT	Q9jk11 rattus norv
2	913	98.7	199	1	RTN4_MOUSE	Q99p72 mus musculu
3	908	98.2	1192	1	RTN4_HUMAN	Q9nqc3 homo sapien
4	679	73.4	776	1	RTN1_HUMAN	Q16799 homo sapien
5	678	73.3	777	1	RTN1_RAT	Q64548 rattus norv
6	622.5	67.3	236	1	RTN3_HUMAN	Q95197 homo sapien
7	622.5	67.3	237	1	RTN3_MOUSE	Q9es97 mus musculu
8	475	51.4	545	1	RTN2_HUMAN	Q75298 homo sapien
9	472	51.0	471	1	RTN2_MOUSE	Q70622 mus musculu
10	94	10.2	468	1	ACH5_HUMAN	P30532 homo sapien
11	92.5	10.0	197	1	AR61_DROME	Q9ves1 drosophila
12	88.5	9.6	1278	1	NPC1_HUMAN	Q15118 homo sapien
13	86.5	9.4	578	1	MDLB_BUCBP	Q89a96 buchnera ap
14	86	9.3	589	1	Y015_MYCGE	P47261 mycoplasma
15	85.5	9.2	296	1	YBZ7_YEAST	P38279 saccharomycc
16	85	9.2	299	1	Y779_METJA	Q58189 methanococc
17	83.5	9.0	570	1	SECD_STRCO	Q53955 streptomyce

18	83	9.0	388	1	YUBA_BACSU	032086 bacillus su
19	82.5	8.9	502	1	OXAA_AQUAE	066561 aquifex aeo
20	82	8.9	744	1	PRES_RAT	Q9eph0 rattus norv
21	81.5	8.8	499	1	UBPG_YEAST	Q02863 saccharomyc
22	81.5	8.8	580	1	MDLB_BUCAI	P57552 buchnera ap
23	81.5	8.8	839	1	TLR4_PANPA	Q9ttn0 pan paniscu
24	81	8.8	607	1	GLMS_AGRT5	Q8ueh1 a glucosami
25	81	8.8	744	1	PRES_MERUN	Q9jkq2 meriones un
26	81	8.8	744	1	PRES_MOUSE	Q99nh7 mus musculu
27	79.5	8.6	324	1	MRAY_LISIN	Q929y0 listeria in
28	79.5	8.6	470	1	YMP8_CAEEL	P53993 caenorhabdi
29	79.5	8.6	592	1	Y036_HAEIN	Q57335 haemophilus
30	79	8.5	556	1	NU2M_PODAN	P15578 podospora a
31	78.5	8.5	748	1	TAP1_HUMAN	Q03518 homo sapien
32	78	8.4	284	1	HTPX_METJA	Q59076 methanococc
33	78	8.4	660	1	SGAT_MYCPN	P75291 mycoplasma
34	78	8.4	744	1	PRES_HUMAN	P58743 homo sapien
35	78	8.4	993	1	NISB_LACLA	P20103 lactococcus
36	77.5	8.4	503	1	C72R_ARATH	Q9sael arabidopsis
37	77.5	8.4	780	1	FTSK_SPOUR	Q9rnvl sporosarcin
38	77.5	8.4	1277	1	NPC1_PIG	P56941 sus scrofa
39	77	8.3	329	1	O5T2_HUMAN	Q8ngg2 homo sapien
40	77	8.3	839	1	TLR4_HUMAN	Q00206 homo sapien
41	76.5	8.3	526	1	ERGL_HUMAN	Q9hat1 homo sapien
42	76	8.2	312	1	OLF2_CHICK	P37068 gallus gall
43	76	8.2	666	1	NU5M_CHOCR	P48920 chondrus cr
44	75.5	8.2	221	1	YA78_AQUAE	Q67171 aquifex aeo
45	75.5	8.2	554	1	PIGS_HUMAN	Q96s52 homo sapien

ALIGNMENTS

RESULT 1

RTN4_RAT

ID RTN4_RAT STANDARD; PRT; 1163 AA.
 AC Q9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
 DE (Glut4 vesicle 20 kDa protein).
 GN RTN4 OR NOGO.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
 RX MEDLINE=99249816; PubMed=10231557;
 RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
 RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:
 RT a new member of the reticulon family.";
 RL Biochim. Biophys. Acta 1450:68-76(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RX MEDLINE=20129258; PubMed=10667796;
RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
RA Spillmann A.A., Christ F., Schwab M.E.:
RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
RT antigen for monoclonal antibody IN-1.";
RL Nature 403:434-439(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
RA Ito T., Schwartz S.M.;
RT "Cloning of a member of the reticulon gene family in rat: one of two
RT minor splice variants.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP FUNCTION.
RX MEDLINE=22033691; PubMed=12037567;
RA GrandPre T., Li S., Strittmatter S.M.;
RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
RL Nature 417:547-551(2002).
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC block the regeneration of the nervous central system in adults (By
CC similarity).
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xL and Bcl-2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC membrane of the endoplasmic reticulum through 2 putative
CC transmembrane domains (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=Nogo-A, NI-220-250;
CC IsoId=Q9JK11-1; Sequence=Displayed;
CC Name=2; Synonyms=Nogo-B, Foocen-M1;
CC IsoId=Q9JK11-2; Sequence=VSP_005658;
CC Name=3; Synonyms=Nogo-C, VP20;
CC IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
CC Name=4; Synonyms=Foocen-M2;
CC IsoId=Q9JK11-4; Sequence=VSP_005659;
CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
CC present in dorsal root ganglion, sciatic nerve and PC12 cells
CC after longer exposure. Isoforms 2 and 3 are detected in kidney,
CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high
CC level in skeletal muscle. In adult animals isoform 1 is expressed
CC mainly in the nervous system.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF051335; AAF01564.1; -.
DR EMBL; AJ242961; CAB71027.1; -.
DR EMBL; AJ242962; CAB71028.1; -.

DR EMBL; AJ242963; CAB71029.1; -.
 DR EMBL; AF132045; AAD31019.1; -.
 DR EMBL; AF132046; AAD31020.1; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
 DR GO; GO:0005635; C:nuclear membrane; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
 DR GO; GO:0030517; P:negative regulation of axon extension; ISS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT DOMAIN 1 989 CYTOPLASMIC (Potential).
 FT TRANSMEM 990 1010 POTENTIAL.
 FT DOMAIN 1011 1104 LUMENAL (Potential).
 FT TRANSMEM 1105 1125 POTENTIAL.
 FT DOMAIN 1126 1163 CYTOPLASMIC (Potential).
 FT DOMAIN 976 1163 RETICULON.
 FT DOMAIN 33 46 POLY-GLU.
 FT DOMAIN 73 76 POLY-ALA.
 FT DOMAIN 140 145 POLY-PRO.
 FT VARSPLIC 1 964 Missing (in isoform 3).
 /FTId=VSP_005656.
 FT VARSPLIC 965 975 AVLSAELSKTS -> MDGQKKHWKDK (in isoform 3).
 /FTId=VSP_005657.
 FT VARSPLIC 173 975 Missing (in isoform 2).
 /FTId=VSP_005658.
 FT VARSPLIC 192 975 Missing (in isoform 4).
 /FTId=VSP_005659.
 FT CONFLICT 1130 1131 MISSING (IN REF. 3; AAD31020).
 SQ SEQUENCE 1163 AA; 126386 MW; 8CB894B09E94F0B6 CRC64;

Query Match 100.0%; Score 925; DB 1; Length 1163;
 Best Local Similarity 100.0%; Pred. No. 1.2e-68;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAA	60
Db	975	SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAA	1034
Qy	61	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV	120
Db	1035	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV	1094
Qy	121	LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK	180
Db	1095	LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK	1154
Qy	181	IPGLKRKAD 189	
Db	1155	IPGLKRKAD 1163	

RESULT 2

RTN4_MOUSE

ID RTN4_MOUSE STANDARD; PRT; 199 AA.

AC Q99P72; Q9CTE3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
GN RTN4 OR NOGO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3T3-L1; TISSUE=Adipocyte;
RA Coulson A.C., Craggs P.D., Morris N.J.;
RT "Mouse vp20/RTN4C cDNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 170-199 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC block the regeneration of the nervous central system in adults (By
CC similarity).
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xL and Bcl-2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC membrane of the endoplasmic reticulum through 2 putative
CC transmembrane domains (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms may be produced;
CC Name=1;
CC IsoId=Q99P72-1; Sequence=Displayed;
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
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CC -----
DR EMBL; AF326337; AAK08076.1; -.
DR EMBL; AK003859; -; NOT_ANNOTATED_CDS.
DR MGD; MGI:1915835; Rtn4.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
DR GO; GO:0005635; C:nuclear membrane; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT DOMAIN 1 25 CYTOPLASMIC (Potential).
FT TRANSMEM 26 50 POTENTIAL.
FT DOMAIN 51 137 LUMENAL (Potential).
FT TRANSMEM 138 162 POTENTIAL.
FT DOMAIN 163 199 CYTOPLASMIC (Potential).
FT DOMAIN 12 199 RETICULON.
SQ SEQUENCE 199 AA; 22466 MW; 07BE5D580059ED9C CRC64;

Query Match 98.7%; Score 913; DB 1; Length 199;
Best Local Similarity 98.9%; Pred. No. 2e-68;
Matches 186; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 12 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAVL 121
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAVL 131

Qy 122 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 132 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 191

Qy 182 PGLKRKAD 189
||| ||| :
Db 192 PGLKRKAE 199

RESULT 3

RTN4_HUMAN

ID RTN4_HUMAN STANDARD; PRT; 1192 AA.
AC Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;
AC Q9Y5U6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
GN RTN4 OR NOGO OR ASY OR KIAA0886.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20129242; PubMed=10667780;
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
RA Michalovich D., Simmons D.L., Walsh F.S.;
RT "Inhibitor of neurite outgrowth in humans.";
RL Nature 403:383-384(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=21010696; PubMed=11126360;
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
endoplasmic reticulum and reduces their anti-apoptotic activity.";
RL Oncogene 19:5736-5746(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20237542; PubMed=10773680;
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
2p14-->2p13 by radiation hybrid mapping.";
RL Cytogenet. Cell Genet. 88:101-102(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RA Jin W.-L., Ju G.;
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Placenta, and Skeletal muscle;
RA Ito T., Schwartz S.M.;
RT "Cloning of a member of the reticulon gene family in human.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fibroblast;
RA Yutsudo M.;
RT "Isolation of a cell death-inducing gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Pituitary;
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
RA Luo B., Hu R., Chen J.;
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,

RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel human cDNA clone with function of inhibiting cancer cell
RT growth.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [11]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=20499367; PubMed=11042152;
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.";
RL Genome Res. 10:1546-1560(2000).
RN [12]
RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
RC TISSUE=Brain;
RA Mao Y.M., Xie Y., Zheng Z.H.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN [13]
RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;

RA Sha J.H., Zhou Z.M., Li J.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN [14]
RP TOPOLOGY.
RC TISSUE=Brain;
RX MEDLINE=20129259; PubMed=10667797;
RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
RT "Identification of the Nogo inhibitor of axon regeneration as a
RT Reticulon protein.";
RL Nature 403:439-444(2000).
RN [15]
RP FUNCTION.
RC TISSUE=Brain;
RX MEDLINE=21069055; PubMed=11201742;
RA Fournier A.E., Grandpre T., Strittmatter S.M.;
RT "Identification of a receptor mediating Nogo-66 inhibition of axonal
RT regeneration.";
RL Nature 409:341-346(2001).
RN [16]
RP REVIEW.
RX MEDLINE=21888956; PubMed=11891768;
RA Ng C.E.L., Tang B.L.;
RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
RT regeneration.";
RL J. Neurosci. Res. 67:559-565(2002).
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC block the regeneration of the nervous central system in adults.
CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xL and Bcl-2.
CC This is likely consecutive to their change in subcellular
CC location, from the mitochondria to the endoplasmic reticulum,
CC after binding and sequestration.
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xL and Bcl-2.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum. Anchored to the membrane of the endoplasmic reticulum
CC through 2 putative transmembrane domains.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
CC IsoId=Q9NQC3-1; Sequence=Displayed;
CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
CC IsoId=Q9NQC3-2; Sequence=VSP_005655;
CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
CC IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
CC Name=4;
CC IsoId=Q9NQC3-4; Sequence=VSP_005654;
CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
CC and testis and weakly in heart and skeletal muscle. Isoform 2 is
CC widely expressed excepted for the liver. Isoform 3 is expressed in
CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-
CC specific.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -!- CAUTION: Ref.11 sequence differs from that shown due to
CC frameshifts in positions 1149 and 1156.
CC -----
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DR EMBL; AJ251383; CAB99248.1; -.
DR EMBL; AJ251384; CAB99249.1; -.
DR EMBL; AJ251385; CAB99250.1; -.
DR EMBL; AB040462; BAB18927.1; -.
DR EMBL; AB040463; BAB18928.1; -.
DR EMBL; AF148537; AAG12176.1; -.
DR EMBL; AF148538; AAG12177.1; -.
DR EMBL; AF087901; AAG12205.1; -.
DR EMBL; AF320999; AAG40878.1; -.
DR EMBL; AF132047; AAD31021.1; -.
DR EMBL; AF132048; AAD31022.1; -.
DR EMBL; AB015639; BAA83712.1; -.
DR EMBL; AF077050; AAD27783.1; -.
DR EMBL; AF177332; AAG17976.1; -.
DR EMBL; AB020693; BAA74909.1; -.
DR EMBL; BC001035; AAH01035.1; -.
DR EMBL; BC007109; AAH07109.1; -.
DR EMBL; BC014366; AAH14366.1; -.

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Query Match      98.2%;  Score 908;  DB 1;  Length 1192;
Best Local Similarity 97.4%;  Pred. No. 3.2e-67;
Matches 184;  Conservative 3;  Mismatches 2;  Indels 0;  Gaps 0;
```

Qy	1	SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA	60
Db	1004	SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA	1063
Qy	61	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFVDDLVDSDLKFAV	120
Db	1064	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFVDDLVDSDLKFAV	1123
Qy	121	LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK	180
		:	
Db	1124	LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK	1183
Qy	181	IPGLKRKAD	189
		:	
Db	1184	IPGLKRKAE	1192

RESULT 4

RTN1 HUMAN

ID RTN1 HUMAN STANDARD; PRT; 776 AA.

AC Q16799; Q16800; Q16801;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

PT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Reticulon 1

GN RTN1 OR NSP.

OS *Homo sapiens* (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).
RC TISSUE=Lung carcinoma;
RX MEDLINE=93293865; PubMed=7685762;
RA Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V.,
RA Ramaekers F.C.S., Van de Ven W.J.M.;
RT "Cloning and expression of alternative transcripts of a novel
RT neuroendocrine-specific gene and identification of its 135-kDa
RT translational product.";
RL J. Biol. Chem. 268:13439-13447(1993).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=96429995; PubMed=8833145;
RA Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,
RA Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;
RT "Genomic organization of the human NSP gene, prototype of a novel gene
RT family encoding reticulons.";
RL Genomics 32:191-199(1996).
RN [3]
RP TISSUE SPECIFICITY.
RX MEDLINE=98228245; PubMed=9560466;
RA Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,
RA Roebroek A.J., van de Velde H.J.K., Ramaekers F.C., Broers J.L.;
RT "Neuronal differentiation is accompanied by NSP-C expression.";
RL Cell Tissue Res. 292:229-237(1998).
CC -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC membrane trafficking in neuroendocrine cells.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=RTN1-A; Synonyms=NSP-A;
CC IsoId=Q16799-1; Sequence=Displayed;
CC Name=RTN1-B; Synonyms=NSP-B;
CC IsoId=Q16799-2; Sequence=VSP_005644;
CC Name=RTN1-C; Synonyms=NSP-C;
CC IsoId=Q16799-3; Sequence=VSP_005645, VSP_005646;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES
CC AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C
CC IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.
CC -!- PTM: Isoforms RTN1-A and RTN1-B are phosphorylated.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
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CC -----
DR EMBL; L10333; AAA59950.1; -.
DR EMBL; L10334; AAA59951.1; -.
DR EMBL; L10335; AAA59952.1; -.
DR PIR; A46583; A46583.
DR PIR; I60904; I60904.
DR Genew; HGNC:10467; RTN1.

DR MIM; 600865; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; TAS.
 DR GO; GO:0004871; F:signal transducer activity; NAS.
 DR GO; GO:0030182; P:neuron differentiation; TAS.
 DR GO; GO:0007165; P:signal transduction; NAS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;
 KW Phosphorylation.
 FT TRANSMEM 603 623 POTENTIAL.
 FT TRANSMEM 726 746 POTENTIAL.
 FT DOMAIN 589 776 RETICULON.
 FT DOMAIN 609 612 POLY-LEU.
 FT VARSPLIC 1 420 Missing (in isoform RTN1-B).
 FT VARSPLIC 1 568 Missing (in isoform RTN1-C).
 FT VARSPLIC 569 588 GPGPLGPAPPPLFLNKQK -> MQATADSTKMDCVWSNW
 KSQ (in isoform RTN1-C).
 FT VARSPLIC 569 588 /FTId=VSP_005646.
 SQ SEQUENCE 776 AA; 83617 MW; CA5B6232353096FE CRC64;

 Query Match 73.4%; Score 679; DB 1; Length 776;
 Best Local Similarity 67.9%; Pred. No. 1.6e-48;
 Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

 Qy 3 VDLLYWRDIKKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
 ::|||||:||:||:|:| ||| ||| ||:|| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :|||:
 Db 590 IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVAYLALAALSATISFRIYKSVLQAVQ 649

 Qy 63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
 ||:|||||:||| ||: :||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
 Db 650 KTDEGHPFKAYLELEITLSQEIQKYTDCQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 709

 Qy 123 WVFTYVGALFNGLTLLLALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
 ||: ||| ||| ||| ||| ||| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 710 WLLTYVGALFNGLTLLMAVVSMTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 769

 Qy 183 GLKRKAD 189
 ||| |:
 Db 770 GAKRHAE 776

RESULT 5
 RTN1_RAT
 ID RTN1_RAT STANDARD; PRT; 777 AA.
 AC Q64548; Q64547;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reticulon 1 (Neuroendocrine-specific protein) (S-rex).
 GN RTN1 OR NSP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).
 RC STRAIN=Wistar; TISSUE=Brain cortex;
 RX MEDLINE=96386034; PubMed=8793864;
 RA Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,
 RA Georgiev G.P., Buchman V.L.;
 RT "Intracellular compartmentalization of two differentially spliced s-
 RT rex/NSP mRNAs in neurons.";
 RL Mol. Cell. Neurosci. 7:289-303(1996).
 CC -!- FUNCTION: May be involved in neuroendocrine secretion or in
 CC membrane trafficking in neuroendocrine cells.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=RTN1-B; Synonyms=S-RexB;
 CC IsoId=Q64548-1; Sequence=Displayed;
 CC Name=RTN1-S; Synonyms=S-RexS;
 CC IsoId=Q64548-2; Sequence=VSP_005647, VSP_005648;
 CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND
 CC PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS
 CC HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
 CC EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL
 CC TYPES.
 CC -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE
 CC HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC
 CC DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN
 CC THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB
 CC DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE
 CC HINDBRAIN.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; U17604; AAC53046.1; -.
 DR EMBL; U17603; AAC53045.1; -.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT TRANSMEM 604 624 POTENTIAL.
 FT TRANSMEM 727 747 POTENTIAL.
 FT DOMAIN 590 777 RETICULON.
 FT DOMAIN 610 613 POLY-LEU.
 FT VARSPLIC 1 569 Missing (in isoform RTN1-S).
 FT /FTId=VSP_005647.
 FT VARSPLIC 570 589 IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW
 FT KSQ (in isoform RTN1-S).
 FT /FTId=VSP_005648.
 SQ SEQUENCE 777 AA; 83001 MW; AF7479C50F28D0AC CRC64;

Query Match 73.3%; Score 678; DB 1; Length 777;
 Best Local Similarity 67.4%; Pred. No. 1.9e-48;
 Matches 126; Conservative 32; Mismatches 29; Indels 0; Gaps 0;

Qy 3 VDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
 :|||||||||:|||:|||: | || ||| ||:||| ||:||| || ||||||| ||:|||:
 Db 591 IDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVAYLALAALSATISFRIYKSVLQAVQ 650

Qy 63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAVLM 122
 |:|||||||:|||: |: :|||: :|||: :|||:||||||||| |||||||||:
 Db 651 KTDEGHPFKAYLELEITLSQEIQKYTDCLQLYVNSTIKELRRFLVQDLVDLSLKFAVLM 710

Qy 123 WVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
 |: |||||||||:|||:||:||:||:|||:|||:|||:|||:|||:|||:
 Db 711 WLLTYVGALFNGLTLMAVVSMTLPVYYVKHQAQVDQYLGLVRTHINTVVAKIQAKIP 770

Qy 183 GLKRKAD 189
 | || |:
 Db 771 GAKRHAE 777

RESULT 6

RTN3_HUMAN

ID RTN3_HUMAN STANDARD; PRT; 236 AA.
 AC O95197;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like
 DE protein II) (NSPLII).
 GN RTN3 OR NSPL2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Retina;
 RX MEDLINE=99265974; PubMed=10331947;
 RA Moreira E.F., Jaworski C.J., Rodriguez I.R.;
 RT "Cloning of a novel member of the reticulon gene family (RTN3): gene
 RT structure and chromosomal localization to 11q13.";
 RL Genomics 58:73-81(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou Y., Du G., Yuan J., Qiang B.;
 RT "Cloning and expression analysis of a cDNA encoding a novel
 RT neuroendocrine-specific protein-like protein 1: NSPL1.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Eye, and Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Potential).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
CC BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL
CC RETINA.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
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CC -----
DR EMBL; AF059524; AAC99319.1; -.
DR EMBL; AF059529; AAD20951.1; -.
DR EMBL; AF059525; AAD20951.1; JOINED.
DR EMBL; AF059526; AAD20951.1; JOINED.
DR EMBL; AF059527; AAD20951.1; JOINED.
DR EMBL; AF059528; AAD20951.1; JOINED.
DR EMBL; AF119297; AAD26810.1; -.
DR EMBL; BC000634; AAH00634.1; -.
DR EMBL; BC010556; AAH10556.1; -.
DR EMBL; BC011394; AAH11394.1; -.
DR EMBL; BC022993; AAH22993.1; -.
DR Genew; HGNC:10469; RTN3.
DR MIM; 604249; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Transmembrane; Endoplasmic reticulum.
FT TRANSMEM 68 88 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
FT DOMAIN 48 236 RETICULON.
SQ SEQUENCE 236 AA; 25609 MW; DDC6A4544ABCDFB7 CRC64;

Query Match 67.3%; Score 622.5; DB 1; Length 236;
Best Local Similarity 59.5%; Pred. No. 2.1e-44;
Matches 113; Conservative 41; Mismatches 35; Indels 1; Gaps 1;

QY	1	SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA	60
	: : : : : : : :		
Db	47	AVHDLIFWRDVKKTGFGTTLIMLLSLAAFSVISVSYLILALLSVTISFRIYKSVIQA	106
QY	61	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLKFAV	120
	: : : : :: : : : : : : :		
Db	107	VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFIVEDLVDSLKLAV	166
QY	121	LMWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK	180
	: : : : : : ::: : :		
Db	167	FMWLMTYVGAVFNGITLLILAEELLIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAK	226
QY	181	IPGL-KRKAD	189
	: : : :		
Db	227	LPGIAKKKAE	236

RESULT 7

RTN3_MOUSE

ID	RTN3_MOUSE	STANDARD;	PERT;	237 AA.
AC	Q9ES97;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Reticulon protein 3.			
GN	RTN3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;			
RT	"Cloning and expression profile of a novel mouse cDNA encoding a human			
RT	RTN3 homolog.";			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF195940; AAG31360.1; -.
 DR EMBL; BC014697; AAH14697.1; -.
 DR MGD; MGI:1339970; Rtn3.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Transmembrane; Endoplasmic reticulum.
 FT TRANSMEM 69 89 POTENTIAL.
 FT TRANSMEM 167 187 POTENTIAL.
 FT DOMAIN 49 237 RETICULON.
 SQ SEQUENCE 237 AA; 25428 MW; EB60A0A7AC45F0DE CRC64;

 Query Match 67.3%; Score 622.5; DB 1; Length 237;
 Best Local Similarity 59.5%; Pred. No. 2.1e-44;
 Matches 113; Conservative 41; Mismatches 35; Indels 1; Gaps 1;

 Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
 Db 48 AVHDLIFWRDVKKTGFVFGTTLIMLLSAAFSVISVSYLILALLSVTISFRVYKSVIQA 107

 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAV 120
 Db 108 VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHVNKALKLIIRFLVEDLVDSLKLA 167

 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
 Db 168 FMWLMTYVGAVFNGITLLILAEELLVFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAK 227

 Qy 181 IPGL-KRKAD 189
 Db 228 LPGIAKKKAE 237

RESULT 8
 RTN2_HUMAN
 ID RTN2_HUMAN STANDARD; PRT; 545 AA.
 AC 075298; 060509;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like

DE protein 1) (NSPL1).
GN RTN2 OR NSPL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC TISSUE=Lung carcinoma;
RX MEDLINE=98360096; PubMed=9693037;
RA Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;
RT "cDNA cloning, genomic organization, and expression of the human RTN2
gene, a member of a gene family encoding reticulons.";
RL Genomics 51:98-106(1998).
RN [2]
RP SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).
RC TISSUE=Brain;
RX MEDLINE=98191726; PubMed=9530622;
RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
RT "Molecular cloning of a novel mouse gene with predominant muscle and
neural expression.";
RL Mamm. Genome 9:274-282(1998).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=RTN2-A;
CC IsoId=075298-1; Sequence=Displayed;
CC Note=Isoform RTN2-C is produced by alternative initiation at
CC Met-341 of isoform RTN2-A;
CC Name=RTN2-B;
CC IsoId=075298-2; Sequence=VSP_005649;
CC Event=Alternative initiation;
CC Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced
CC by alternative initiation at Met-1 and Met-341;
CC -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL
CC MUSCLE.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
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CC -----
DR EMBL; AF004222; AAC32542.1; -.
DR EMBL; AF004223; AAC32543.1; -.
DR EMBL; AF004224; AAC32544.1; -.
DR EMBL; AF038540; AAC14910.1; -.
DR Genew; HGNC:10468; RTN2.
DR MIM; 603183; -.
DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; NAS.
DR GO; GO:0004871; F:signal transducer activity; NAS.
DR GO; GO:0007165; P:signal transduction; NAS.
DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;
 KW Alternative initiation.
 FT CHAIN 1 545 RETICULON PROTEIN 2, ISOFORM RTN2-A.
 FT CHAIN 341 545 RETICULON PROTEIN 2, ISOFORM RTN2-C.
 FT INIT_MET 341 341 FOR ISOFORM RTN2-C.
 FT TRANSMEM 368 388 POTENTIAL.
 FT TRANSMEM 463 483 POTENTIAL.
 FT DOMAIN 345 545 RETICULON.
 FT VARSPLIC 272 344 Missing (in isoform RTN2-B).
 FT /FTId=VSP_005649.
 SQ SEQUENCE 545 AA; 59263 MW; 971FD2F909E1E9E6 CRC64;

 Query Match 51.4%; Score 475; DB 1; Length 545;
 Best Local Similarity 50.5%; Pred. No. 7e-32;
 Matches 92; Conservative 36; Mismatches 54; Indels 0; Gaps 0;

 Qy 2 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAQI 61
 | |||||:| : :||| : ||| ||||||| :||| ||| :||:| :||| :||| :|||:
 Db 345 VADLLYWKDTRTSGVVFTGLMVSLLCLLHFSIVSVAHLALLLCGTISLRVYRKVLQAV 404

 Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
 : | :||:|||: : :| :| :| :|| :||| :||| :||| :|||:
 Db 405 HRGDGANPFQAYLDVDLTLTREQTERLSHQITSRVVSAATQLRHFFLVEDLVDSLKLALL 464

 Qy 122 MWVFTYVGALFNGLTLILALISLFSIPVYIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
 :: |:|||:|||||:||| :| ||:|||:| :||| :||| :||| :|||:
 Db 465 FYILTFVGAIFNGLTLILGVIGLFTIPLLYRQHQQIDQYVGLVTNQLSHIKAKIRAKI 524

 Qy 182 PG 183
 ||
 Db 525 PG 526

RESULT 9

RTN2_MOUSE
 ID RTN2_MOUSE STANDARD; PRT; 471 AA.
 AC 070622; 070620;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like
 DE protein 1) (NSPL1).
 GN RTN2 OR NSPL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
 RC STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;
 RX MEDLINE=98191726; PubMed=9530622;
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
 RT "Molecular cloning of a novel mouse gene with predominant muscle and
 RT neural expression.";
 RL Mamm. Genome 9:274-282(1998).

RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Retina;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
CC (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Brain;
CC IsoId=070622-1; Sequence=Displayed;
CC Name=2; Synonyms=Muscle;
CC IsoId=070622-2; Sequence=VSP_005650, VSP_005651;
CC -!- TISSUE SPECIFICITY: Expressed predominantly in neural and muscular
CC tissues.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
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CC -----
DR EMBL; AF038537; AAC14906.1; -.
DR EMBL; AF038537; AAC14907.1; -.
DR EMBL; AF038538; AAC14908.1; -.
DR EMBL; AF038539; AAC14909.1; -.
DR EMBL; AF093624; AAD13195.1; -.
DR EMBL; BC031370; AAH31370.1; -.
DR MGD; MGI:107612; Rtn2.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT TRANSMEM 295 315 POTENTIAL.
FT DOMAIN 272 471 RETICULON.

FT VARSPLIC 1 267 Missing (in isoform 2).
 FT /FTId=VSP_005650.
 FT VARSPLIC 268 271 PLLL -> MGSK (in isoform 2).
 FT /FTId=VSP_005651.
 SQ SEQUENCE 471 AA; 51346 MW; 9BBD8F372CF63AD3 CRC64;

 Query Match 51.08; Score 472; DB 1; Length 471;
 Best Local Similarity 48.9%; Pred. No. 1.1e-31;
 Matches 89; Conservative 39; Mismatches 54; Indels 0; Gaps 0;

 QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
 | |||||:| : :| || : || | ||||| ||::|| | ||| |:|: |::|:
 Db 272 VADLLYWKDTRTSGAVFTGLMASLLCLLHFSIVSVAHLALLGLCATISLRVYRKVLQAV 331

 QY 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
 : | :||:||: :: :: | :: | || || :|| | ||:||||| ||:|:
 Db 332 HRGDGTNPQAYLMDMLTLTREQTERLSQQIASHVVSTATQLRHFFLVEDLVDSLKLALL 391

 Qy 122 MWVFTYVGALFNGLTLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
 :: |:||:|||||:|| ::||:||:||:| :|| ||| |:|| : | ||:||:
 Db 392 FYILTFVGAIFNGLTLVILGVVALFTVPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKI 451

 Qy 182 PG 183
 ||
 Db 452 PG 453

RESULT 10

ACH5_HUMAN

ID ACH5_HUMAN STANDARD; PRT; 468 AA.
 AC P30532; Q15824; Q99554;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-5 chain precursor.
 GN CHRNA5 OR NACHRA5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92179225; PubMed=1542648;
 RA Chini B., Clementi F., Hukovic N., Sher E.;
 RT "Neuronal-type alpha-bungarotoxin receptors and the alpha 5-nicotinic
 receptor subunit gene are expressed in neuronal and nonneuronal human
 cell lines.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1572-1576(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97062879; PubMed=8906617;
 RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
 RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
 RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
 2-beta 4 nicotinic acetylcholine receptor subunits and functional
 expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
 beta 4 subunits.";

RL J. Mol. Neurosci. 7:217-228 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97162233; PubMed=9009220;
RA Groot Kormelink P.J., Luyten W.H.M.L.;
RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
RT expression of seven nAChR subunits in the human neuroblastoma cell
RT line SH-SY5Y and/or IMR-32.";
RL FEBS Lett. 400:309-314 (1997).
RN [4]

RP SEQUENCE FROM N.A.
RA Duga S., Solda G., Asselta R., Bonati M.T., Dalpra L., Malcovati M.,
RA Tenchini M.L.;
RT "Characterization of the genomic structure of human nicotinic
RT acetylcholine receptor CHRNA5/A3/B4 gene cluster: identification of
RT two novel introns in the 3' untranslated region of CHRNA3 and of a
RT tail-to-tail overlap between CHRNA3 and CHRNA5.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

RN [5]
RP SEQUENCE FROM N.A.

RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Neuronal AChR seems to be composed of two different type
CC of subunits: alpha and non-alpha (beta).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.

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CC -----

DR EMBL; M83712; AAA58357.1; -.

DR EMBL; U62434; AAB40112.1; -.

DR EMBL; Y08419; CAA69696.1; -.

DR EMBL; AJ306481; CAC34820.1; -.

DR EMBL; AJ306482; CAC34820.1; JOINED.

DR EMBL; AJ306483; CAC34820.1; JOINED.

DR EMBL; AJ306484; CAC34820.1; JOINED.

DR EMBL; AJ306485; CAC34820.1; JOINED.

DR EMBL; AJ306486; CAC34820.1; JOINED.

DR EMBL; BC033639; AAH33639.1; -.

DR PIR; A38223; A38223.

DR Genew; HGNC:1959; CHRNA5.

DR MIM; 118505; -.

DR InterPro; IPR006029; Neu_channel_memb.

DR InterPro; IPR006202; Neur_chan_LBD.

DR InterPro; IPR006201; Neur_channel.

DR Pfam; PF02931; Neur_chan_LBD; 1.

DR Pfam; PF02932; Neur_chan_memb; 1.

DR PRINTS; PR00252; NRIONCHANNEL.

DR TIGRFAMs; TIGR00860; LIC; 1.

DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.

KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;

KW Transmembrane; Multigene family.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 468 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 ALPHA-5 CHAIN.

FT DOMAIN 23 249 EXTRACELLULAR.

FT TRANSMEM 250 274 POTENTIAL.

FT TRANSMEM 282 299 POTENTIAL.

FT TRANSMEM 316 337 POTENTIAL.

FT DOMAIN 338 429 CYTOPLASMIC.

FT TRANSMEM 430 448 POTENTIAL.

FT DISULFID 170 184 BY SIMILARITY.

FT DISULFID 234 235 ASSOCIATED WITH RECEPTOR ACTIVATION
 (BY SIMILARITY).

FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 23 34 RCGLAGAAAGGAQ -> ALRSSRARRAAR (IN REF. 1).

FT CONFLICT 128 128 V -> S (IN REF. 1).

FT CONFLICT 365 365 C -> S (IN REF. 1).

FT CONFLICT 398 398 D -> N (IN REF. 2 AND 4).

FT CONFLICT 405 405 R -> T (IN REF. 1).

SQ SEQUENCE 468 AA; 53054 MW; 7FE91A2E362289C0 CRC64;

Query Match 10.2%; Score 94; DB 1; Length 468;
 Best Local Similarity 21.5%; Pred. No. 1.5;
 Matches 41; Conservative 32; Mismatches 62; Indels 56; Gaps 7;

Qy 24 LLLSLTVFSIV-----SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP- 69
 :|:||||| :| :| :| :| :| :| :| :| :|

Db 288 VLVSLTVFLLVIEEIIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTFAINIHHRSSSTHNA 347

Qy 70 -----FRAYLESEVAISEELVQ---KYSNSALGHVNSTIKELRRLF 107

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL *Science* 287:2185-2195(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the ARL6ip family.

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CC -----

DR EMBL; AE003714; AAF55348.1; -.
DR FlyBase; FBgn0038453; CG10326.

KW Transmembrane.

FT TRANSMEM 43 63 POTENTIAL.
FT TRANSMEM 64 84 POTENTIAL.
FT TRANSMEM 129 149 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
SQ SEQUENCE 197 AA; 22233 MW; 7D35ABAD18CE272E CRC64;

Query Match 10.0%; Score 92.5; DB 1; Length 197;
Best Local Similarity 24.6%; Pred. No. 0.83;
Matches 48; Conservative 24; Mismatches 80; Indels 43; Gaps 8;

Qy 5 LLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFR-----IYKGV 57
Db :|| | ||||| || || : :|| | ::|: :::: |: ||
Qy 32 VLTWEKQYYAGVVFGVISCLYLVLWYLDLSLITLLSLLGVISILLNYAFPMVSRLIFGGV 91
Db
Qy 58 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSDLK 117
Db |: | | |: || | || | ||: |:: | |||
Qy 92 ---NWDGDQEAKFEDVCGQVCAVKGSLLVWY-EYLFNERKSTV-----FVI---VMSLG 138
Db
Qy 118 FAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAK- 176
Db : | :||: | | |: || : : | || || : |: :
Qy 139 LLAMAW---IGAIINNLLMYLATLLIIMWP-----GLQNKDIFKAITQR 180
Db
Qy 177 ----IQAKIPGLKRK 187
Db | || | |||
Qy 181 ASKIIINEKIQCGKRK 195

RESULT 12

NPC1_HUMAN

ID NPC1_HUMAN STANDARD; PRT; 1278 AA.
AC O15118; Q9P130;
DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Niemann-Pick C1 protein precursor.
GN NPC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS NPC1.
RX MEDLINE=97362323; PubMed=9211849;
RA Carstea E.D., Morris J.A., Coleman K.G., Loftus S.K., Zhang D.,
RA Cummings C., Gu J., Rosenfeld M.A., Pavan W.J., Krizman D.B.,
RA Nagle J., Polymeropoulos M.H., Sturley S.L., Ioannou Y.A.,
RA Higgins M.E., Comly M., Cooney A., Brown A., Kaneski C.R.,
RA Blanchette-Mackie E.J., Dwyer N.K., Neufeld E.B., Chang T.-Y.,
RA Liscum L., Strauss J.F. III, Ohno K., Zeigler M., Carmi R., Sokol J.,
RA Markie D., O'Neill R.R., van Diggelen O.P., Elleder M.,
RA Patterson M.C., Brady R.O., Vanier M.T., Pentchev P.G., Tagle D.A.;
RT "Niemann-Pick C1 disease gene: homology to mediators of cholesterol
RT homeostasis.";
RL Science 277:228-231(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS.
RX MEDLINE=99355599; PubMed=10425213;
RA Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G.,
RA Carstea E.D.;
RT "The genomic organization and polymorphism analysis of the human
RT Niemann-Pick C1 gene.";
RL Biochem. Biophys. Res. Commun. 261:493-498(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21623216; PubMed=11754101;
RA Bauer P., Knoblich R., Bauer C., Finckh U., Hufn A., Kropp J.,
RA Braun S., Kustermann-Kuhn B., Schmidt D., Harzer K., Rolfs A.;
RT "NPC1: Complete genomic sequence, mutation analysis, and
RT characterization of haplotypes.";
RL Hum. Mutat. 19:30-38(2002).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99128318; PubMed=9927649;
RA Watari H., Blanchette-Mackie E.J., Dwyer N.K., Glick J.M., Patel S.,
RA Neufeld E.B., Brady R.O., Pentchev P.G., Strauss J.F. III;
RT "Niemann-Pick C1 protein: obligatory roles for N-terminal domains and
RT lysosomal targeting in cholesterol mobilization.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:805-810(1999).
RN [5]
RP VARIANT NPD TRP-992.
RX MEDLINE=98299797; PubMed=9634529;
RA Greer W.L., Riddell D.C., Gillan T.L., Girouard G.S., Sparrow S.M.,
RA Byers D.M., Dobson M.J., Neumann P.E.;
RT "The Nova Scotia (type D) form of Niemann-Pick disease is caused by a
RT G3097-->T transversion in NPC1.";
RL Am. J. Hum. Genet. 63:52-54(1998).
RN [6]
RP VARIANTS NPC1 GLN-934; LEU-940; ASN-948; LEU-954; TRP-992; ALA-1007;
RP THR-1061 AND VAL-1213.

RX MEDLINE=99452586; PubMed=10521290;
RA Greer W.L., Dobson M.J., Girouard G.S., Byers D.M., Riddell D.C.,
RA Neumann P.E.;
RT "Mutations in NPC1 highlight a conserved NPC1-specific cysteine-rich
RT domain.";
RL Am. J. Hum. Genet. 65:1252-1260(1999).
RN [7]
RP VARIANT NPC1 THR-1061.
RX MEDLINE=99452593; PubMed=10521297;
RA Millat G., Marcais C., Rafi M.A., Yamamoto T., Morris J.A.,
RA Pentchev P.G., Ohno K., Wenger D.A., Vanier M.T.;
RT "Niemann-Pick C1 disease: the I1061T substitution is a frequent mutant
RT allele in patients of Western European descent and correlates with a
RT classic juvenile phenotype.";
RL Am. J. Hum. Genet. 65:1321-1329(1999).
RN [8]
RP VARIANTS NPC1, AND VARIANTS ARG-215; VAL-858 AND GLN-1266.
RX MEDLINE=99408226; PubMed=10480349;
RA Yamamoto T., Nanba E., Ninomiya H., Higaki K., Taniguchi M., Zhang H.,
RA Akaboshi S., Watanabe Y., Takeshima T., Inui K., Okada S., Tanaka A.,
RA Sakuragawa N., Millat G., Vanier M.T., Morris J.A., Pentchev P.G.,
RA Ohno K.;
RT "NPC1 gene mutations in Japanese patients with Niemann-Pick disease
RT type C.";
RL Hum. Genet. 105:10-16(1999).
RN [9]
RP VARIANTS NPC1 GLN-958 AND ALA-1007.
RX MEDLINE=21313111; PubMed=11349231;
RA Sun X., Marks D.L., Park W.D., Wheatley C.L., Puri V., O'Brien J.F.,
RA Kraft D.L., Lundquist P.A., Patterson M.C., Pagano R.E., Snow K.;
RT "Niemann-Pick C variant detection by altered sphingolipid trafficking
RT and correlation with mutations within a specific domain of NPC1.";
RL Am. J. Hum. Genet. 68:1361-1372(2001).
RN [10]
RP VARIANTS NPC1 ALA-378; MET-950; ARG-992 AND THR-1061.
RX MEDLINE=21313105; PubMed=11333381;
RA Millat G., Marcais C., Tomasetto C., Chikh K., Fensom A.H., Harzer K.,
RA Wenger D.A., Ohno K., Vanier M.T.;
RT "Niemann-Pick C1 disease: correlations between NPC1 mutations, levels
RT of NPC1 protein, and phenotypes emphasize the functional significance
RT of the putative sterol-sensing domain and of the cysteine-rich
RT luminal loop.";
RL Am. J. Hum. Genet. 68:1373-1385(2001).
RN [11]
RP VARIANTS NPC1 TYR-177; CYS-978 AND VAL-1035.
RX MEDLINE=21372069; PubMed=11479732;
RA Ribeiro I., Marcaio A., Amaral O., Sa Miranda M.C., Vanier M.T.,
RA Millat G.;
RT "Niemann-Pick type C disease: NPC1 mutations associated with severe
RT and mild cellular cholesterol trafficking alterations.";
RL Hum. Genet. 109:24-32(2001).
CC -!- FUNCTION: Involved in the intracellular trafficking of
CC cholesterol. May play a role in vesicular trafficking in glia, a
CC process that may be crucial for maintaining the structural and
CC functional integrity of nerve terminals.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Found in late
CC endosomes and lysosomes.

CC -!- DOMAIN: A cysteine-rich N-terminal domain and a C-terminal domain
CC containing a di-leucine motif necessary for lysosomal targeting
CC are critical for mobilization of cholesterol from lysosomes.
CC -!- PTM: Glycosylated.
CC -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease
CC type C1 (NPC1) [MIM:257220]. NPC1 is an autosomal recessive lipid
CC storage disorder, which affects particularly the brain, liver and
CC spleen, and which is characterized by lysosomal accumulation of
CC low density lipoprotein derived cholesterol. Clinical features
CC include variable hepatosplenomegaly and severe progressive
CC neurological dysfunction such as ataxia, dystonia and dementia.
CC The age of onset can vary from infancy to late adulthood.
CC -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease
CC type D (NPD) [MIM:257250]; also known as Niemann-Pick disease
CC without sphingomyelinase deficiency, or Nova Scotian type. Because
CC of evidence from biochemical changes, lack of complementation, and
CC linkage mapping to the same chromosome site, NPD and NPC1 are
CC considered to be allelic disorders.
CC -!- SIMILARITY: Belongs to the patched family.
CC -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.

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CC -----

DR EMBL; AF002020; AAB63982.1; -.
DR EMBL; AF157379; AAD48006.1; -.
DR EMBL; AF157365; AAD48006.1; JOINED.
DR EMBL; AF157366; AAD48006.1; JOINED.
DR EMBL; AF157367; AAD48006.1; JOINED.
DR EMBL; AF157368; AAD48006.1; JOINED.
DR EMBL; AF157369; AAD48006.1; JOINED.
DR EMBL; AF157370; AAD48006.1; JOINED.
DR EMBL; AF157371; AAD48006.1; JOINED.
DR EMBL; AF157372; AAD48006.1; JOINED.
DR EMBL; AF157373; AAD48006.1; JOINED.
DR EMBL; AF157374; AAD48006.1; JOINED.
DR EMBL; AF157375; AAD48006.1; JOINED.
DR EMBL; AF157376; AAD48006.1; JOINED.
DR EMBL; AF157377; AAD48006.1; JOINED.
DR EMBL; AF157378; AAD48006.1; JOINED.
DR EMBL; AF338230; AAK25791.1; -.
DR EMBL; AF123046; AAF28875.1; -.
DR EMBL; AF123045; AAF28875.1; JOINED.
DR Genew; HGNC:7897; NPC1.
DR MIM; 607623; -.
DR MIM; 257220; -.
DR MIM; 257250; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005764; C:lysosome; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0005478; F:intracellular transporter activity; TAS.
DR GO; GO:0015248; F:sterol transporter activity; TAS.

DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
 DR InterPro; IPR004765; NP_C_type.
 DR InterPro; IPR003392; Patched.
 DR InterPro; IPR000731; SSD_5TM.
 DR Pfam; PF02460; Patched; 1.
 DR TIGRFAMs; TIGR00917; 2A060601; 1.
 DR PROSITE; PS50156; SSD; 1.
 KW Signal; Glycoprotein; Transmembrane; Lysosome; Polymorphism;
 KW Disease mutation.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 1278 NIEMANN-PICK C1 PROTEIN.
 FT TRANSMEM 270 290 POTENTIAL.
 FT TRANSMEM 351 371 POTENTIAL.
 FT TRANSMEM 622 642 POTENTIAL.
 FT TRANSMEM 655 675 POTENTIAL.
 FT TRANSMEM 678 698 POTENTIAL.
 FT TRANSMEM 760 780 POTENTIAL.
 FT TRANSMEM 833 853 POTENTIAL.
 FT TRANSMEM 1099 1119 POTENTIAL.
 FT TRANSMEM 1125 1145 POTENTIAL.
 FT TRANSMEM 1196 1216 POTENTIAL.
 FT TRANSMEM 1228 1248 POTENTIAL.
 FT DOMAIN 249 259 POLY-PRO.
 FT DOMAIN 620 785 SSD.
 FT SITE 1275 1278 DI-LEUCINE MOTIF.
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL)

```

Query Match          9.6%;  Score 88.5;  DB 1;  Length 1278;
Best Local Similarity 25.7%;  Pred. No. 12;
Matches 39;  Conservative 25;  Mismatches 51;  Indels 37;  Gaps 7;
y          46 SVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR 105
b          ::|||||  :: :  :: : |  |  |  ||  :: | : ||||  ||  ||
598 NLTISFTAERSIEDELNRESDSDVF-----TVVISYAIMFLYISLALGH---IKSCRR 647
y          106 LFLVDD-----LVDSLKFAVLMWVFTYVGALFNGLTLLALI-----SLF 146
b          | |||           |:  |  : ||:||:|  |||::: :|  ::|
648 L-LVDSKVSLGIAGILIVLSSVACSLGVFESYIGL---PLTLIVIEVIPFLVLAVGVDNIF 703
y          147 SIPVIYERHQ---VQIDHYLGLANKSVKDAM 174
b          :  |:| :  ::|  ||  |  :|
704 ILVQAYORDERLQGETLDQQQLGRVLGEVAPSM 735

```

RESULT 13
MDLB_BUCBP
ID MDLB_BUCBP STANDARD; PRT; 578 AA.
AC Q89A96;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Multidrug resistance-like ATP-binding protein mdlB.
GN MDLB OR BBP424.
OS Buchnera aphidicola (subsp. *Baizongia pistaciae*).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI TaxID=135842;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426901; PubMed=12522265;
 RA Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
 RA Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,
 RA Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
 RT "Reductive genome evolution in Buchnera aphidicola.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.
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 CC -----
 DR EMBL; AE014017; AAO27134.1; -.
 DR InterPro; IPR001140; ABC_TM_transpt.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00664; ABC_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR PROSITE; PS50929; ABC_TM1F; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Transport; Transmembrane; Complete proteome.
 FT TRANSMEM 26 46 POTENTIAL.
 FT TRANSMEM 59 79 POTENTIAL.
 FT TRANSMEM 143 163 POTENTIAL.
 FT TRANSMEM 166 186 POTENTIAL.
 FT TRANSMEM 196 216 POTENTIAL.
 FT TRANSMEM 260 280 POTENTIAL.
 FT DOMAIN 339 573 ABC TRANSPORTER.
 FT NP_BIND 373 380 ATP (POTENTIAL).
 SQ SEQUENCE 578 AA; 66827 MW; 3B84848CE196ADF7 CRC64;

 Query Match 9.4%; Score 86.5; DB 1; Length 578;
 Best Local Similarity 19.9%; Pred. No. 7.8;
 Matches 43; Conservative 46; Mismatches 72; Indels 55; Gaps 10;

 Qy 1 SVVD-----LLYWRDIKKGVVFGASLFLLLSL-----TV-FS 32
 :|:| |||: | :: | :| | |: || :|
 Db 3 NVIDFWPTLKRLLYGTNVKKYLILGFTLLLSSIEVLPILISCFIKHYFINNTVNYS 62

 Qy 33 IVSVTAYIALALLSVTISF-----RIYKGVIQA---IQKSDEGHPFRAYLESEVAIS 81
 : :| |: | :|: ::| :| ||| : | | | : : : : :|
 Db 63 LKIITYYLILQILAAILNYHQNIIFNKISLTIVIQLRYDMSSTLQLPIKMFQDQPIG-- 120

 Qy 82 EELVQKYSNSALGHVNSTIKEL-----RRLF--LVDDLVDSDLKFAVLMWVFTYVGALFNG 134
 : : : :| ||||| : || :: |: : :| | : :| :| :|
 Db 121 -QFISRITND----TETIKELYDTVIKSLFQNIILILITLITMFILEWRMACIASIIFP 174

 Qy 135 LTLLLALISLFSIPVIYERHQVQIDHYLGLANKSV 170
 : |:|: | || |:: :| | : :| :| :|:
 Db 175 IALIIMLLYQYFSKPIL-RKIKVYIANIYNIFNEII 209

RESULT 14

Y015_MYCGE

ID Y015_MYCGE STANDARD; PRT; 589 AA.

AC P47261;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical ABC transporter ATP-binding protein MG015.

GN MG015.

OS Mycoplasma genitalium.

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

OX NCBI_TaxID=2097;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33530 / G-37;

RX MEDLINE=96026346; PubMed=7569993;

RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

RT "The minimal gene complement of Mycoplasma genitalium.";

RL Science 270:397-403(1995).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- SIMILARITY: Belongs to the ABC transporter family. MsbA subfamily.

CC -----

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CC -----

DR EMBL; U39680; AAC71231.1; -.

DR PIR; F64201; F64201.

DR HSSP; P13569; 1NBD.

DR TIGR; MG015; -.

DR InterPro; IPR003593; AAA_ATPase.

DR InterPro; IPR001140; ABC_TM_transpt.

DR InterPro; IPR003439; ABC_transporter.

DR Pfam; PF00664; ABC_membrane; 1.

DR Pfam; PF00005; ABC_tran; 1.

DR ProDom; PD000006; ABC_transporter; 1.

DR SMART; SM00382; AAA; 1.

DR PROSITE; PS50929; ABC_TM1F; 1.

DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.

DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.

KW Hypothetical protein; ATP-binding; Transport; Transmembrane;

KW Complete proteome.

FT TRANSMEM 9 29 POTENTIAL.

FT TRANSMEM 66 86 POTENTIAL.

FT TRANSMEM 161 181 POTENTIAL.

FT TRANSMEM 251 271 POTENTIAL.

FT TRANSMEM 280 300 POTENTIAL.
 FT TRANSMEM 303 323 POTENTIAL.
 FT NP_BIND 385 392 ATP (POTENTIAL).
 SQ SEQUENCE 589 AA; 66126 MW; 0EA6A816DD3A3CC9 CRC64;

 Query Match 9.3%; Score 86; DB 1; Length 589;
 Best Local Similarity 22.7%; Pred. No. 8.8;
 Matches 45; Conservative 40; Mismatches 71; Indels 42; Gaps 7;

 Qy 3 VDILLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
 || :| :: :| : :|| |||||| ::| ||:| :| :| || :| :| :| :|
 Db 48 VDSIY-----SLIYPTNLNVFIRLT---IVSVTVFVAYALIFVFNVAQNYVG-IKLYQ 96

 Qy 63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLF-----LVDDLVDSDL 116
 :: :| :| : : : : : : : : : : : || :| :| :|
 Db 97 QTCATLRWKAYLKMQSMSTSFFDTQNNGDLMSRLNDMYNIDNLFTQAGGQAIQSLFNIL 156

 Qy 117 KFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYER---HQVQ----- 158
 :|:|:|:|:|:| || :| :| :| :| :| :| :|
 Db 157 TTSVLIFLLSPVIAL---ISLSILATLITFSFAFLKKSKTYSQVQNNLGDMMSGYIEEVL 213

 Qy 159 ---IDHYLGLANKSVKD 172
 :| :| :| :|
 Db 214 TNHKVVHVVLKLQEIMIKD 231

RESULT 15
YBZ7_YEAST
ID YBZ7_YEAST STANDARD; PRT; 296 AA.
AC P38279;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 33.5 kDa protein in MRPS9-YSW1 intergenic region.
GN YBR147W OR YBR1124.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Entian K.-D., Koetter P., Rose M., Becker J., Grey M., Li Z.,
RA Niegemann E., Schenk-Groeninger R., Servos J., Wehner E.,
RA Wolter R., Brendel M., Bauer J., Braun H., Dern K., Duesterhus S.,
RA Gruenbein R., Hedges D., Kiesau P., Korol S., Krems B., Proft M.,
RA Siegers K., Baur A., Boles E., Miosga T.,
RA Schaaff-Gerstenschlaeger I., Zimmermann F.K.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: SOME, TO S.POMBE SPAC2E12.03C AND SPAC17C9.10.
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CC -----
DR EMBL; Z36016; CAA85105.1; -.
DR PIR; S46018; S46018.
DR GermOnline; 138690; -.
DR SGD; S0000351; YBR147W.
DR InterPro; IPR006603; CTNS.
DR Pfam; PF04193; PQ-loop; 2.
DR SMART; SM00679; CTNS; 2.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 13 33 POTENTIAL.
FT TRANSMEM 45 65 POTENTIAL.
FT TRANSMEM 69 89 POTENTIAL.
FT TRANSMEM 164 184 POTENTIAL.
FT TRANSMEM 200 220 POTENTIAL.
FT TRANSMEM 239 259 POTENTIAL.
FT TRANSMEM 263 283 POTENTIAL.
SQ SEQUENCE 296 AA; 33496 MW; 50D65896A1BAFB43 CRC64;

Query Match 9.2%; Score 85.5; DB 1; Length 296;
Best Local Similarity 29.3%; Pred. No. 4.7;
Matches 41; Conservative 17; Mismatches 55; Indels 27; Gaps 7;

Qy 17 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY---KGVIQAIQKS-DEGH--- 68
| || : || :: : || || | : | | | :: | :: | | |
Db 61 VMGAMMQNLLP---TMIILAAYYTLADLILLIQCWYDKEKKSILOEVKKNVDPVHLPP 116
Qy 69 -----PFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD-- 115
| | | | || | ||: || : || | | | | | | : |
Db 117 ANPINETVLQDVFNEYEPPLLPRIEEEDSQSYSSLELGR-TIVVKE-RENFFNDLIVSGV 174
Qy 116 LKFAVLMWVFTYVGALFNGL 135
| : | | : | | ||:
Db 175 LIAGILSWYISYCSGLDNGI 194

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